

—

Db 61 FVAELKANDINWVELIDLVAETDYLASQAEAKDKLIEBFLDSBPVLSEEHKVVVRNFLKA 120  
QY 121 KPT-HEMVFEFMSGITYKVELGVSENELIVDPMPNLVFTTRDPFASVNGVYTIHPWRYIVR 179  
Db 121 KTSRKLVNIMAGITKYDGLIEADHELIVDPMPNLVFTTRDPFASVNGVYTIHPWRYKVR 180  
QY 180 RRETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLDITL 239  
Db 181 QRETLFSRFVSNHPKLVNTWYDPSIKLSIEGDDVFIYNNETLVVGVSERTDLDITL 240  
QY 240 LAKNIKANKVEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSPDIANDVFKFWDYDLV 299  
Db 241 LAKNIVANKCEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSPDIANDVFKFWDYDLV 300  
QY 300 NGGAEPOPOLNGLPLDKLLASIIINKEPVLPIPGAGATEMEIARETFNFDGTYNLAIKPGL 359  
Db 301 NGGAEPOPOLNGLPLDKLLASIIINKEPVLPIPGAGATEMEIARETFNFDGTYNLAIRPGV 360  
QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVKW 409  
Db 361 VIGYSRNEKTNAALEAGIKVLPFHGNQLSLGMGNARCMSPLSRKDVVKW 410

RESULT 2  
S68515  
A:Title: probable arginine deiminase (EC 3.5.3.6) - Mycoplasma arginini (fragment)  
C:Species: Mycoplasma arginini  
C>Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 07-Dec-1999  
C:Accession: S68515; S68514  
R:WilM, M.; Shevchenko, A.; Houthaeve, T.; Breit, S.; Schweigerer, L.; Fotsis, T.; Mann, Nature 379, 466-469, 1996  
A:Title: Femtomole sequencing of proteins from polyacrylamide gels by nano-electrospray  
A:Reference number: S68514; MUID:96158883; PMID:8559255  
A:Accession: S68515  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-410 <WIL>  
A:Cross-references: EMBL:X93471  
A:Note: only a part of the translation is shown  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995  
A:Accession: S68514  
A:Note: only a part of the translation is shown  
A:Note: peptides obtained by mass spectrometry  
C:Genetics:  
A:Genetic code: SGC3  
C:Superfamily: arginine deiminase arca  
C:Keywords: hydrolase

Query Match 80.3%; Score 1702.5; DB 2; Length 410;  
Best Local Similarity 78.3%; Pred. No. 4.6e-113;  
Matches 321; Conservative 48; Mismatches 40; Indels 1; Gaps 1;  
QY 1 MSVPDSKFNHGVYSEIGELETVLVHPGKEIDYITPARLDELFSAILSHDARKEHQ 60  
Db 1 MSVPDSKFNHGVYSEIGELETVLVHPGKEIDYITPARLDELFSAILSHDARKEHQ 60  
QY 61 FVKIMKORGINVELTDLVAETDYLASQAEAKDKLIEBFLDSBPVLSEEHKVVVRNFLKA 120  
Db 61 FVEILKQGINVELVDPVWETYNLVKTKQELKDLFDLSDSEPLVSPHKKAVKEFLKS 120  
QY 121 -KPTHEMVFEFMSGITYKVELGVSENELIVDPMPNLVFTTRDPFASVNGVYTIHPWRYIVR 179  
Db 121 LKSTKELIYMMAGITKYDGLIEADHELIVDPMPNLVFTTRDPFASVNGVYTIHPWRYKVR 180  
QY 180 RRETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLDITL 239  
Db 181 QRETLFSKFIPTNHPKLVKTPWYDPAKMPISIEGDDVFIYNNETLVVGVSERTDLDITL 240  
QY 240 LAKNIKANKVEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSPDIANDVFKFWDYDLV 299  
Db 241 LAKNIKANKCEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSPDIANDVFKFWDYDLV 300

QY 300 NGGAEPOPOLNGLPLDKLLASIIINKEPVLPIPGAGATEMEIARETFNFDGTYNLAIKPGL 359  
Db 301 NGGAEPOPOLNGLPLDKLLASIIINKEPVLPIPGAGATEMEIARETFNFDGTYNLAIKPGL 360  
QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVKW 409  
Db 361 VIGYSRNEKTNAALEANGIKVLPFHGNQLSLGMGNARCMSPLSRKDVVKW 410

RESULT 3  
A38835  
streptococcal antitumor protein - Streptococcus pyogenes  
C:Species: Streptococcus pyogenes  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
C:Accession: A38835; A33225; S16694  
R:kanaoka, M.; Kawanaka, C.; Negoro, T.; Fukita, Y.; Taya, K.; Agui, H. Agric. Biol. Chem. 51, 2641-2648, 1987  
A:Title: Cloning and expression of the antitumor glycoprotein gene of Streptococcus pyogenes  
A:Reference number: JE0061  
A:Accession: A38835  
A:Molecule type: DNA  
A:Residues: 1-411 <KAN>  
A:Cross-references: UNIPROT:P16962; EMBL:X55659; NID:g47340; PIDN:CAA39192.1; PID:g47341  
R:kanaoka, M.; Negoro, T.; Kawanaka, C.; Agui, H.; Nabeshima, S. Agric. Biol. Chem. 55, 743-750, 1991  
A:Title: Streptococcal antitumor protein: expression in Escherichia coli cells and properties  
A:Reference number: JH0364; MUID:91234346; PMID:1368629  
A:Accession: A33225  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-57 <KA2>  
C:Superfamily: arginine deiminase arca

Query Match 32.0%; Score 679; DB 2; Length 411;  
Best Local Similarity 39.4%; Pred. No. 1.5e-40;  
Matches 163; Conservative 70; Mismatches 155; Indels 26; Gaps 10;  
QY 11 IHVYSEIGELETVLVHPGKEIDYITPARLDELFSAILSHDARKEHQSFVKIMKDRGI 70  
Db 7 IHVYSEIGKUKVLLHHPGKEINLMPDYLERLLFDDIPLEDAQKEHDAPALDEGI 66  
QY 71 NVVELTDLVAETDYLASQAEAKKEFIETFLBEETVPLTEANKKAVRAPLLS-KPTHEMVFE 129  
Db 67 EVLYLETAAES--LVTPEIREAPIDEVLYSE-ANIRGRATKKAIRELLMAIEDNQELIEK 123  
QY 130 MMSGITKYELG-----VESENELIVDPMPNLVFTTRDPFASVNGVYTIHPWRYI 177  
Db 124 TWAGVQKSELPEIPASEKGLTDLVESNYPPAIDMPNLVFTTRDPFATIGTGSNLHMFSE 183  
QY 178 VRRETLFARFVRNHPKLV--VKTWPYDPAKMPIEGGDVFIYNNETLVVGVSERTDLD 235  
Db 184 TRRETLVYKGIYTHPIYGGKVPWYDRNETRIEGGDELVLSDKDLVAVGISORTDAA 243  
QY 236 TITLAKNIKANKVEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSP-IANDVFKFW 294  
Db 244 SIEKLLVNI-FKQNLGPKKVLAFEPANRRKFMHLDITVFMVDYDKFTIHPHIEIGDLRV-- 300  
QY 295 DYDLVNGGAEPOPOLNGLPLDKLLASIIINKEPV-LPIPGAGATEMEIARETFNFDGTYN 353  
Db 301 -YSVTYDNEHLHIVBEKGLDLAEALLAANLGVKEDVLDLRCGGDNL--VAAGREQWNDGSNTL 357  
QY 354 AIKPGGLVIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDV 407  
Db 358 TIAPGVVVVYNNRTIITNAILSEKGLKLIKHSGLVGRGGPRCMSPFPFEREDI 411

RESULT 4  
D95251  
arginine deiminase [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: D95251  
R:Tettelin, H.; Nelson, K.B.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide

Matches	148;	Conservative	85;	Mismatches	155;	Indels	27;	Gaps	10;
Qy	11	IHYVSIGLETVLVHHPGREIDYITPARDELFLSAILSHDARKEHSFVKIMKDORGI	70						
Dd	6	IKVNSBIGALKTKVLKRPKGLENLVPDYLDGLGDDIPYLEVAQAKHEHDHFAQVLRBEGV	65						
Qy	71	NVVVELTDLVAEVDYLSKAQAEEFIETFEETVPVLTEANKKAVRAPLLSKPTHEMVPEPM	130						
Dd	66	EVLVLEKLAAES--IENPQVRSEFIDDLAASKTIL-GHEEIEKITLFATLSNQELVDKI	122						
Qy	131	MSGITTYELG-----VESNELIVDPMPNLYFTDRDPFASVGNGVTTHFMRYIVRRR	181						
Dd	123	MSGVRKEENPKCTHLVEYMDDKPYFLDPMPNLYFTDRDPAQSIGHGITINRMFRARRR	182						
Qy	182	ETLPAPFVFNRHPKL--VKTPTYDYDPAMKMPIEGGDVFIYNNTLVVGVSERDTLDTITL	239						
Dd	183	ESIFIQIVVXKHPRFKDANIPIWLDRCPPNIEGGDELVLSKDVLAIGVSERTSAQAIEK	242						
Qy	240	LAKNIKANKEVEKRVAINVPKWTNLMLHTLTWLMDKNKP-LYSPIAN-----DVFKE	293						
Dd	243	LARRIFENPOATPKKVVAIBIPTSRTFMHLDTVFTMIDYDKFTMHSAILKAEGNMNIP-I	301						
Qy	294	WDYDLVNGGAEPQQLNGLPLDKLLASIINKSPV-LIPIGCAGATEMEIARETNFDGTNY	352						
Dd	302	IEYDVVNKDIAIKSSH---LKDTLEDVLGIDDIQIFPTGNDV--IDGAREQNWDGSNT	356						
Qy	353	LAIKPGLVIGYDRNEKTNAALKAAGITVLPFHGNQLSLGMGNARCWSMPIRSKXDV	407						
Dd	357	LCIRPGVVVTRYDRNVSYNDLLRQKGIKVIISGSELVGRGGPCRCMSQPLFREDI	411						
RESULT 6									
AE1437									
arginine deiminase homolog lin0036 [imported] - Listeria innocua (strain Clip11)									
C:Species: Listeria innocua									
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004									
C:Accession: AE1437									
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Jones, L.M.; Karst, U.									
Science 294, 849-852, 2001									
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournon, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.H.; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Jones, L.M.; Karst, U.									
A;Title: Comparative genomics of Listeria species.									
A;Reference number: AB1077; PMID:21537279; PMID:11679669									
A;Accession: AE1437									
A>Status: preliminary									
A:Molecule type: DNA									
A;Residues: 1-408 <GLA>									
A;Cross-references: UNIPROT:Q92FR7; CB:AL592022; PIDN:CAC95269.1; PID:g16412457									
A;Experimental source: strain Clip11262									
C:Genetics:									
A;Gene: lin0036									
C;Superfamily: arginine deiminase arca									
Query Match 30.1%; Score 638; DB 2; Length 408;									
Best Local Similarity 38.5%; Pred. No. 1.2e-37;									
Matches 161; Conservative 74; Mismatches 153; Indels 30; Gaps 11;									
Qy	9	NGHVSVSEIGELETVLVHEPGRIDVITPARDELFLSAILSHDARKEHQSFVKIMKDR	68						
Dd	3	NGLNITSEIGKQTVLVRFSGSENIITPEYLSLLFDDI.PYLKMMMQKEDHFVKTQWDS	62						

Db 177 PARRRESFIELLKHHPFSSQBIPIWSGREPPFLEGGDELILNBETVLVGVSRDTA 236

Qy 235 DTITLLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSP-IANDVPFK 293

Db 237 RAVERLABSL-FSRAPKIKRVLAAEIPETRSFMHLDTVTFVWNPFAQFTIHPAIQOQOEL 295

Qy 294 WDYDL--VNGGAEPQPOLNGLPLDKLASIINKEPV-LIPIGGAGATEMETARETNDGT 350

Db 296 NVYILEKSENGLEITPRRD---FKRVIAEVLGVPEVDFIPCGGBDV--IVSAREQWMDGA 350

Qy 351 NYLAIKPOLVICYDRNEKTNAAKAGITVLPFFHGNOLSLGMGNARCMSPLSRKDVK 408

Db 351 NTLAIPGEVITYDRNVHSNDLLRKAGIKVHEVISSELSRGGPRCMTWPIITGNLK 408

RESULT 7

AD1080

arginine deiminase homolog lmo0043 [imported] - Listeria monocytogenes (strain EGD-e)

C:Species: Listeria monocytogenes

C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004

C:Accession: AD1080

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloesker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mak, C.; Schluecker, T.; Smoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AD1080

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-410 <G>

A:Cross-references: UNIPROT:Q8VASO; GB:NC\_003210; PIDN:CAC98258.1; PID:g16409402; GSPDB:AD1080

A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: lmo0043

C:Superfamily: arginine deiminase arca

Query Match 29.8%; Score 632; DB 2; Length 410;

Best Local Similarity 37.5%; Pred. No. 3.2e-37;

Matches 156; Conservative 78; Mismatches 152; Indels 30; Gaps 11;

Qy 11 IHVYSEIGELTVLHPGRIDYITPARDELIFSAILSHDARKEHQSFVKIMKDRGI 70

Db 7 LNTISEIGKQTVLVKRGSELENITPEYLESLLFDDIPYLKMKQKSHDFFAKTRDSNI 66

Qy 71 NVBELTDLVAETVYDLASKAAKEEFITFLEETVPVLTANKKA--VRAFLLSKPTHEMVE 128

Db 67 EVLYLEKLAEAALREANN--KESFLTKIKES----NQMDSEALYVRDYLMSFDEEEMIR 120

Qy 129 FMSGIGTKYELGVSENEL-----IVDPMPNLYFTRDPPFASGVNGVTIHFMYIY 178

Db 121 KLMSGKKSETPERKKKHLNEMDMEQYFFFLDPLNLYFTRDPAAVIENGVTINRMFQPA 180

Qy 179 RRETLFARFVRNHPKLVK--TPWYDPAKMPIEGDDVFIYNNETLVGVSERTDLD 236

Db 181 RRRESIFIELLKHHPFSSQBIPIWSGREPPFLEGGDELVLNNEETVLVGVSERTDARA 240

Qy 237 ITLLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSP-IANDVPFKWD 295

Db 241 VERLAESL-FNRSPKIKRVLAVEIPETRSFMHLDTVTFVWNPFAQFTIHPAIQOQOELNI 299

Qy 296 YDL--VNGGAEPQPOLNGLPLDKLASIINKEPV-LIPIGGAGATEMETARETNDGTNY 352

Db 300 YILEKSENGLEITPRRD---FQRVIAEVLDEPFDIFPCGGBDV--IVSAREQWMDGANT 354

Qy 353 LAIKPGVIGYDRNEKTNAAKAGITVLPFHGNOLSLGMGNARCMSPLSRKDVK 408

Db 355 LAIAPGEVITYDRNVHSNDLLRSAGIKVHEVISSELSRGGPRCMTWPIVLENLK 410

RESULT 8

E86879

arginine deiminase [EC 3.5.3.6] [imported] - Lactococcus lactis subsp. lactis (strain ILJ)

C:Species: Lactococcus lactis subsp. lactis

C>Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004

C:Accession: E86879

R:Bohlooin, A.; Wincker, P.; Mauger, S.; Jallion, O.; Malarne, K.; Weissenbach, J.; Ehrlich, S.

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis

A:Reference number: AB6625; MUID:21235186; PMID:11337471

A:Accession: E86879

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-410 <S>

A:Cross-references: UNIPROT:P58013; GB:AE005176; PID:g12725086; PIDN:AAK06135.1; GSPDB:GN

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: arca

C:Superfamily: arginine deiminase arca

C:Keywords: hydrolase

Query Match 29.8%; Score 631.5; DB 2; Length 410;

Best Local Similarity 37.3%; Pred. No. 3.4e-37;

Matches 156; Conservative 70; Mismatches 163; Indels 29; Gaps 6;

Qy 9 NGIHVYSEIGELTVLHPGRIDYITPARDELIFSAILSHDARKEHQSFVKIMKDR 68

Db 3 NGINVNSEIGKLSVILLHRPGEVENITPTMKQLLFDIPYLKIAQKEHDFFAQTLRDN 62

Qy 69 GINWVELTDLVAETVYDLASKAAKEEFITFLEES-----TVPVLTANKKAVRAFLLSK 121

Db 63 GAETVYENLATEVFEKSE--TKEEFLSHLLHAGVRPGTYDGLTE-----YLTSM 113

Qy 122 PTHMVEFMMSGITKVEL-----GVSENELIVDPMPNLYFTRDPPFASGVNGVT 170

Db 114 STKDMYKIVAGYKKNELDKRTALSDMAGSDAENFYLNPLFNAYFTRDPPQASMGVMT 173

Qy 171 IHEWYIVRRRETLFARFVRNHPKLVKTPWYDPAKMPIEGDDVFIYNNETLVGVSE 230

Db 174 INKOTFPARQPESLITYYVWANHPRFKDTPIMWRNHTTRIEGGDELILNKTITVAIGVSE 233

Qy 231 RTDLDTITLLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSP-IANDV 290

Db 234 RTSKTIQNLAKELFANPLSTFDTVLAVEIPHNHMHLDTVTFMINHDQFTVFPFGIMDG 293

Qy 291 FXFDVDLVNGGAEPQPOLNGL-PLDKLASIINKEPVLIPIGAGATEMETARETNFDG 349

Db 294 AGNINVFILRPGKDDSEIHEHLTDLKAALKKVLNLSLSELDLIECGAG-DPIAAPREQWNDG 352

Qy 350 TNYLAIKPGVIGYDRNEKTNAAKAGITVLPFHGNOLSLGMGNARCMSPLSRKDV 407

Db 353 SNTLAIPGEIVTYDRNYVTVELLKEHGKIKVHEILSELGRGGRCMSQPLWREDL 410

RESULT 9

T46741

arginine deiminase [EC 3.5.3.6] [validated] - Lactobacillus sakei

C:Species: Lactobacillus sakei

C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004

C:Accession: T46741

R:Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez, C.

J. Bacteriol. 180, 4154-4159, 1998

A:Title: Structural and functional analysis of the gene cluster encoding the enzymes of the

A:Reference number: 223141; MUID:98361904; PMID:9696763

A:Accession: T46741

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-409 <Z>

A:Cross-references: UNIPROT:O53088; EMBL:AJ001330; NID:g2764610; PIDN:CAA04682.1; PID:927

C:Genetics:

A:Gene: arca

C:Function:

A:Description: EC 3.5.3.6 [validated, MUID:98361904]

A:Pathway: arginine catabolism



A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AB1060

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-406 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD06927.1; PID:g16505575; GSPDB:GN00176

C;Genetics:

A;Gene: STV4805

C;Superfamily: arginine deiminase arca

C;Keywords: hydrolase

Query Match 25.0%; Score 531; DB 2; Length 406;

Best Local Similarity 32.9%; Pred. No. 4.4e-30;

Matches 136; Conservative 74; Mismatches 172; Indels 32; Gaps 9;

Qy 13 VYSEIGLETLVHVEPGRIDYITPARLDELFSAILSHDARKEHOSFVKIMKDRGINV 72

Db 6 VGSBIGQLRSVMLHRPNLSKRLTPSNCQELLFDVLSVERAGEHDFANTLRQOGIEV 65

Qy 73 VELDLVAETDYDLASKAAKEEFIEETFEETVPLTEANKKAVRAFLSKPETHENVEFMS 132

Db 66 LLLDLTLTQTLDVAD--AKAWLLDTQISDY--RLGPTFAADIRAWLADMPHRELARLSG 121

Qy 133 GITKYLGVSESE-----NELIVDPMPNLVYTRDPFASVGVNGVTIHFWRVIYVRRET 183

Db 122 GLTYGEIPASIKNMVVDTHINDIFMKPLPNHLETRDTSCWYNGVSNPMAKPARQRET 181

Qy 184 LFARFVRNHPKLVKTPWY-----YDPAMQPIEGGDVFIYNNETLVVGVSERTDL 234

Db 182 NNLRAIYRWHPQFADGDFIKYFGDENINYDHA---TLEGGDLVIGRGAVLIGNSERTTP 238

Qy 235 DTITLLAKNIKANKVEFKRIYAINVPKWTNLMHLDTWLMDKNKF-LYSPDIANDVFKF 293

Db 239 QGVFLQAALPKHQAB--RVIAVELPKHRSCHMLDTVMTHIDIDTFSVPEVVRPDVQC 296

Qy 294 WDYDLVNGGAPQPLNGLPLDLKLASIINKEPVLIPIGGAGAPEMIAIARETNPDGTNYL 353

Db 297 W--TLTPDGRGLKRTQESTLVHALETALGIDQVRLITTTGDAFEAE--REQNDANNVL 352

Qy 354 AIKPLGVIGYDRNEKTNAAKAGITVLPFHGNQSLGMDGNARCMSPILSRKDV 407

Db 353 TLREPGVVGVYERNITWNEKYDKAGITVLPIDGDLGRGRCGARCSCPLERDGI 406

RESULT 13

F82323

arginine deiminase VC0423 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004

C;Accession: F82323

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: F82323

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-407 <HEI>

A;Cross-references: UNIPROT:Q9KU02; GB:AE004130; GB:AE003852; NID:g9654845; PIDN:AAF9359

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC0423

A;Map position: 1

C;Superfamily: arginine deiminase arca

Query Match 23.7%; Score 502.5; DB 2; Length 407;

Best Local Similarity 31.8%; Pred. No. 4.7e-28;

Matches 134; Conservative 79; Mismatches 171; Indels 37; Gaps 9;

Qy 9 NGIHVYSEIGLETLVHVEPGRIDYITPARLDELFSAILSHDARKEHOSFVKIMKDR 68

Db 2 NRIYVSGVQLRRVILNRPERALTHLTFSNCHLELFDVLAEEAGVEHDAFANTLRQTQ 61

Qy 69 GINVELTDLVAETDYDLASKAAKEEFIEETFEETVPLTEANKKAVRAFLSKPETHEMVE 128

Db 62 DVEVLLHDLLEET--LAIPARQWLLNTQISDFRPGPTFA--RELHALNLHLDHHLTT 117

Qy 129 FMMSGITKYLGVSESE-----ELIVDPMPNLVYTRDPFASVGVNGVTIHFWRVIYVR 179

Db 118 LLGGGLAFSELHLESMLPQMRQPLDFVIEPLNHLFTRDTSCWYGVGVSILNPMKMPAR 177

Qy 180 RRETLFARFVRNHPKLVKTPW-----YDPAMQPIEGGDVFIYNNETLVVGVSE 230

Db 178 QRETNHLRAIYRWHPPIFAQHPFIHYFGIDDLHDVNA---NIEGDDVLVICKGAVLGMSE 234

Qy 231 RTDLDITITLLAKNIKANKVEFKRIYAINVPKWTNLMHLDTWLMDKNKFLYSPDIANDV 290

Db 235 RITSPQGVENLAAL--FKHQASKVIAINLPKHSRCHMLDTVMTHMDVDTFSVYP--EV 289

Qy 291 FKWDYDLVNGGAPQPLNGLPLDLKLASIINKEPVL-----IPIGGAGATEMEIARETN 346

Db 290 MR---KDLPTWRLUTPGNNGDMRVEQVPSYLHAEQALGVLDYLIITTTGNSYEAREQW 346

Qy 347 FDGTNYLAIKPLGVIGYDRNEKTNAAKAGITVLPFHGNQSLGMDGNARCMSPILSRKD 406

Db 347 NDANNVLTVPKGVVIGYERNVYNEKYDKAGIKVLTIPGNELGRGRCGARCSCPIERDG 406

Qy 407 V 407

Db 407 I 407

RESULT 14

S73858

arginine deiminase (EC 3.5.3.6) arca - Mycoplasma pneumoniae (strain ATCC 29342)

N;Alternate names: hypothetical protein H10\_orf238

C;Species: Mycoplasma pneumoniae

A;Variety: ATCC 29342

C;Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 07-Dec-1999

C;Accession: S73858

R;Himmelsreich, R.; Hilbert, H.; Plagens, H.; Pirk, E.; Li, B.C.; Herrmann, R.

Nucleic Acids Res. 24, 4420-4449, 1996

A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae

A;Reference number: S73327; MUID:97105885; PMID:8948633

A;Accession: S73858

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-238 <HIM>

A;Cross-references: EMBL:AB000052; GB:U00089; NID:g1674223; PIDN:AAB96180.1; PID:g1674223

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C;Genetics:

A;Gene: arca

A;Genetic code: SGC3

C;Keywords: hydrolase

Query Match 23.1%; Score 490; DB 2; Length 238;

Best Local Similarity 50.3%; Pred. No. 1.7e-27;

Matches 97; Conservative 43; Mismatches 47; Indels 6; Gaps 3;

Qy 7 KFNHIVYSEIGLETLVHVEPGRIDYITPARLDELFSAILSHDARKEHOSFVKIMK 66

Db 2 KYN-INHVSEIGQLQTLVHTVHTPGNEIRIRISPRRLDLSFSAVIEPDTAQEHQTFQQLQ 60

Qy 67 DRGINVVELTDLVAETDYDLASKAAKEEFIEETFEETVPLTEANKKAVRAFL--SKPT 123

Db 61 EQNIEVVQTLDTATTTFDKANATAQNFITETWLDQAEPLKTPHRRKVAQYLLQEAKST 120

Qy 124 HEMVEFPMMSGITKYLGVSESE--ENELIVDPMPNLVYTRDPFASVGVNGVTIHFWRVIYVR 181

Db 121 LSNVSRMMGMDKRVAAANTINGDFLVDPMNLVYTRDPFASIGHISINRMKYLTRR 180

Qy 182 ETLFARFVRNHP 194

Job time : 44 secs

Db 181 ETLFASFILEPTTP 193

RESULT 15

C95376

probable arginine deiminase (EC 3.5.3.6) [imported] - Sinorhizobium meliloti (strain 102)

C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004

C;Accession: C95376

R;Barnett, M.J.; Fisher, R.P.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows

; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti

A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Accession: C95376

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-419 <KUR>

A;Cross-references: UNIPROT:Q92YG5; GB:AE006469; PIDN:AAK65573.1; PID:g14524052; GSPDB:G

A;Experimental source: strain 1021, megaplasmid pSymA

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebaullt, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: arcA2

A;Genome: plasmid

C;Superfamily: arginine deiminase arca

C;Keywords: hydrolase

Query Match 22.8%; Score 484; DB 2; Length 419;

Best Local Similarity 29.1%; Pred. No. 9.9e-27;

Matches 130; Conservative 82; Mismatches 170; Indels 64; Gaps 14;

QY 1 MSVPDSKFNHIVYSEIGETLVVHEPGREIDYTPARLDLLELSAILESHDARKEHQS 60

Db 1 MSSKSTQHTFFGVHSEVGQURKVMVCAPGRHQRLTPSNCDALEDDVLMVDNARRDHF 60

QY 61 FVKIMKDRGINVVELTDLVAETVDLASKAAKEEFIEFTLEETVP-----VLTEANKKAV 114

Db 61 FMTKMRDRGVEVEMENLLAQT--VAIPARKWILD---NQVVPNQVGLLELDE-----I 110

QY 115 RAFLSKPTHEMVEFMWSGTTKYEL-----GVESNELIVDPMPNLYFT 158

Db 111 RSYLEGLPDRELAETLIGLSTHEFPETHGEMLELIRDAAGVA---EYLLPLPLNTLYT 167

QY 159 RDPFASVGNQVTIHFMYIYVRRETLFARFVRNHPKLV--KTPWYDDPAMK---MPIEG 213

Db 168 RDTTCWYGGVTINPLNYPARHEETILATYKFPDFGVKNVWNGEPTTDWGLATLEG 227

QY 214 GDVFIYNNETLVVGVSERTDLDITLLAKNIKAKKEVEFKRIVAINVPKWTNLMHLDTWL 273

Db 228 GDVMPICKGNVLIGMSERTSRQISQLAATLFEKGAQ--RVIVAAMPKLRAMHLDTVF 285

QY 274 TMLDKN-KFLYSPINDVPKFWDYDLVNGGAEPQQLNGPLDKLLASIN-----K 324

Db 286 TFADRDCLVIYPIDVNEIAF-----SYRPGKPGSLELHKDRGSFVETVRDALGLK 337

QY 325 EPVLIPIGGAGATEMETARETNFD-GTNYLAIKPLGVIGYDRNEKTNAALKAAGITVLPF 383

Db 338 EMRWETG-----NAYVRRTOWDSDGANVCLSPGVVLAYDRNTYNTLLRKAGVEVITI 393

QY 384 HGNQLSLGMGNARCMSPLSRKDKVK 409

Db 394 TGAEIGRGGGHCMTCPPIIRDAVDY 419

Search completed: November 23, 2004, 15:51:55

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2004, 15:45:18 ; Search time 146 Seconds  
(without alignments)  
992.042 Million cell updates/sec

Title: US-10-674-666-1  
Perfect score: 2120  
Sequence: 1 MSVFDKFNHIVSEIGLE.....LQGNARCMPLSRKDKVKW 409

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA:\*  
1: /cgn2\_6/prodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/prodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/prodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/prodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
12: /cgn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/prodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/prodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/prodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/prodata/2/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/prodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2120	100.0	409	16	US-10-674-666-1
2	2116	99.8	409	16	US-10-674-666-2
3	2112	99.6	409	16	US-10-674-666-3
4	2108	99.4	409	16	US-10-674-666-4
5	1797.5	84.8	409	16	US-10-674-666-7
6	1793.5	84.6	409	16	US-10-674-666-9
7	1793.5	84.6	409	16	US-10-674-666-10
8	1789.5	84.4	409	16	US-10-674-666-8
9	1764.5	83.2	410	15	US-10-674-666-5
10	1763.5	83.2	410	15	US-10-343-175-10
11	1760.5	83.0	410	16	US-10-674-666-6
12	707.5	33.4	410	14	US-10-369-493-16696
13	681.5	32.1	413	16	US-10-674-666-19

14	679	32.0	411	16	US-10-674-666-13	Sequence 13, Appl
15	670.5	31.6	408	16	US-10-674-666-20	Sequence 20, Appl
16	655	30.9	413	16	US-10-674-666-18	Sequence 18, Appl
17	651.5	30.7	409	16	US-10-674-666-14	Sequence 14, Appl
18	631.5	29.5	410	14	US-10-369-493-18511	Sequence 18511, A
19	625	29.8	409	16	US-10-674-666-21	Sequence 21, Appl
20	612.5	28.9	410	16	US-10-674-666-15	Sequence 15, Appl
21	600.5	28.3	409	16	US-10-674-666-16	Sequence 16, Appl
22	532	25.1	403	14	US-10-369-493-8351	Sequence 8351, Ap
23	532	25.1	403	14	US-10-369-493-715	Sequence 715, App
24	514	24.2	409	14	US-10-156-761-9857	Sequence 9857, Ap
25	486.5	22.9	418	14	US-10-369-493-13732	Sequence 13732, A
26	476	22.5	399	14	US-10-369-493-7149	Sequence 7149, Ap
27	476	22.5	401	14	US-10-369-493-4394	Sequence 4394, Ap
28	467	22.0	403	14	US-10-369-493-4661	Sequence 4661, Ap
29	457	22.0	403	14	US-10-369-493-7420	Sequence 7420, Ap
30	457	22.0	403	14	US-10-369-493-12226	Sequence 12226, A
31	420	21.6	412	14	US-10-369-493-11106	Sequence 11106, A
32	154	7.3	81	9	US-09-867-550-164	Sequence 164, App
33	136	6.4	105	15	US-10-424-599-164647	Sequence 164647,
34	113.5	5.4	1270	14	US-10-032-585-7127	Sequence 7127, Ap
35	113	5.3	743	15	US-10-282-122A-74773	Sequence 74773, A
36	109	5.1	453	15	US-10-282-122A-42589	Sequence 42589, A
37	105	5.0	580	16	US-10-674-666-17	Sequence 17, Appl
38	104.5	4.9	740	15	US-10-282-122A-72237	Sequence 72237, A
39	104.5	4.9	1057	15	US-10-282-122A-70305	Sequence 70305, A
40	104	4.9	4688	15	US-10-282-122A-76865	Sequence 76865, A
41	103	4.9	502	15	US-10-282-122A-54571	Sequence 54571, A
42	103	4.9	772	13	US-10-121-032-28	Sequence 28, Appl
43	103	4.9	772	14	US-10-093-037-28	Sequence 28, Appl
44	103	4.9	800	14	US-10-228-063-3	Sequence 3, Appl
45	103	4.9	825	14	US-10-228-063-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1  
US-10-674-666-1  
; Sequence 1, Application US/10674666  
; Publication No. US20040131604A1  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Mike A.  
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo  
; FILE REFERENCE: PH050001-300  
; CURRENT APPLICATION NUMBER: US/10/674,666  
; CURRENT FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: US 60/427,497  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Mycoplasma hominus  
US-10-674-666-1

Query Match 100.0%; Score 2120; DB 16; Length 409;  
Best Local Similarity 100.0%; Pred. No. 4.9e-186;  
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSVFDKFNHIVSEIGLETVLVHVEPQREIDYITPARLDELLFSAILESHDARKEHQS	60
DB	1	MSVFDKFNHIVSEIGLETVLVHVEPQREIDYITPARLDELLFSAILESHDARKEHQS	60
QY	61	FKVIMKDRGINVVELTDLVAETIDYDLASKAAKEFIETFTLEETVPVLTEANKKAVRAFLLS	120
DB	61	FKVIMKDRGINVVELTDLVAETIDYDLASKAAKEFIETFTLEETVPVLTEANKKAVRAFLLS	120
QY	121	KPTHEVPEFMSGITYKELGVSENELIVDPNPNLYFTDPDFASVGVNGVTIHFMYIVRR	180
DB	121	KPTHEVPEFMSGITYKELGVSENELIVDPNPNLYFTDPDFASVGVNGVTIHFMYIVRR	180

181 RETLFAFVFRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVSERTDLDITILL 240  
181 RETLFAFVFRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVSERTDLDITILL 240  
241 AKNIKANKEVEFKRIVAINVVKWTNLMHLDTWLMDKNKFLYSPITANDVFKFWDYDLVN 300  
241 AKNIKANKEVEFKRIVAINVVKWTNLMHLDTWLMDKNKFLYSPITANDVFKFWDYDLVN 300  
301 GGAEPQQLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
301 GGAEPQQLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDKVKW 409  
361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDKVKW 409

RESULT 2  
US-10-674-666-2  
; Sequence 2, Application US/10674666  
; Publication No. US20040131604A1  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Mike A.  
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo  
; FILE REFERENCE: PHOE0001-100  
; CURRENT APPLICATION NUMBER: US/10/674,666  
; PRIOR FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: US 60/427,497  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Mycoplasma hominus  
US-10-674-666-2

Query Match 99.8%; Score 2116; DB 16; Length 409;  
Best Local Similarity 99.8%; Pred. No. 1.1e-185;  
Matches 408; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
1 MSVDSKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60  
1 MSVDSKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60  
61 FVKIMKDRGINNVVELTDLVAETDYLASKAAKEEFIEETVLPVLTANKKAVRAFLLS 120  
61 FVKIMKDRGINNVVELTDLVAETDYLASKAAKEEFIEETVLPVLTANKKAVRAFLLS 120  
121 KPTHEWVEFMMSGITKYELGVSENELIVDPMPLNYFTRDPFASVGVNGVTIHFMRIVRR 180  
121 KPTHEWVEFMMSGITKYELGVSENELIVDPMPLNYFTRDPFASVGVNGVTIHFMRIVRR 180  
181 RETLFAFVFRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVSERTDLDITILL 240  
181 RETLFAFVFRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVSERTDLDITILL 240  
241 AKNIKANKEVEFKRIVAINVVKWTNLMHLDTWLMDKNKFLYSPITANDVFKFWDYDLVN 300  
241 AKNIKANKEVEFKRIVAINVVKWTNLMHLDTWLMDKNKFLYSPITANDVFKFWDYDLVN 300  
301 GGAEPQQLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
301 GGAEPQQLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDKVKW 409  
361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDKVKW 409

RESULT 3  
US-10-674-666-3  
; Sequence 3, Application US/10674666

Publication No. US20040131604A1  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Mike A.  
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo  
; FILE REFERENCE: PHOE0001-100  
; CURRENT APPLICATION NUMBER: US/10/674,666  
; CURRENT FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: US 60/427,497  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Mycoplasma hominus  
US-10-674-666-3

Query Match 99.6%; Score 2112; DB 16; Length 409;  
Best Local Similarity 99.8%; Pred. No. 2.7e-185;  
Matches 408; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
1 MSVDSKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60  
1 MSVDSKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60  
61 FVKIMKDRGINNVVELTDLVAETDYLASKAAKEEFIEETVLPVLTANKKAVRAFLLS 120  
61 FVKIMKDRGINNVVELTDLVAETDYLASKAAKEEFIEETVLPVLTANKKAVRAFLLS 120  
121 KPTHEWVEFMMSGITKYELGVSENELIVDPMPLNYFTRDPFASVGVNGVTIHFMRIVRR 180  
121 KPTHEWVEFMMSGITKYELGVSENELIVDPMPLNYFTRDPFASVGVNGVTIHFMRIVRR 180  
181 RETLFAFVFRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVSERTDLDITILL 240  
181 RETLFAFVFRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVSERTDLDITILL 240  
241 AKNIKANKEVEFKRIVAINVVKWTNLMHLDTWLMDKNKFLYSPITANDVFKFWDYDLVN 300  
241 AKNIKANKEVEFKRIVAINVVKWTNLMHLDTWLMDKNKFLYSPITANDVFKFWDYDLVN 300  
301 GGAEPQQLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
301 GGAEPQQLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDKVKW 409  
361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDKVKW 409

RESULT 4  
US-10-674-666-4  
; Sequence 4, Application US/10674666  
; Publication No. US20040131604A1  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Mike A.  
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo  
; FILE REFERENCE: PHOE0001-100  
; CURRENT APPLICATION NUMBER: US/10/674,666  
; CURRENT FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: US 60/427,497  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Mycoplasma hominus  
US-10-674-666-4

Query Match 99.4%; Score 2108; DB 16; Length 409;  
Best Local Similarity 99.5%; Pred. No. 6.2e-185;  
Matches 407; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSVFDKFNKGIHYVSEIGLETVLHVEPGREIDYITPARLDELLFSAILESHDARKEHQS 60  
DB 1 MSVFDKFNKGIHYVSEIGLETVLHVEPGREIDYITPARLDELLFSAILESHDARKEHQS 60  
QY 61 FVKIMKDRGINVVELTDLVAETVDLASKAAKEBFIEFTLEETVPVLTTEANKKAVRAFLLS 120  
DB 61 FVKIMKDRGINVVELTDLVAETVDLASKAAKEBFIEFTLEETVPVLTTEANKKAVRAFLLS 120  
QY 121 KPTHEMVFEFMSGITYELGVSENEELIVDPMNLYFTRDPPASVGVNGVTIHFMRVYVR 180  
DB 121 KPTHEMVFEFMSGITYELGVSENEELIVDPMNLYFTRDPPASVGVNGVTIHFMRVYVR 180  
QY 181 RETLFAFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVVSERTDLDITILL 240  
DB 181 RETLFAFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVVSERTDLDITILL 240  
QY 241 AKNIKANKEVEFKRIVAINVVKWNTNLMHLDITWLTMDKNKFLYSPANDVFKFWDYDLVN 300  
DB 241 AKNIKANKEVEFKRIVAINVVKWNTNLMHLDITWLTMDKNKFLYSPANDVFKFWDYDLVN 300  
QY 301 GGAEPQOLNGLPLDKLASIINKEPVLPIPGGAGATEMEIARETNFDTGNTYLAIKPGLV 360  
DB 301 GGAEPQOLNGLPLDKLASIINKEPVLPIPGGAGATEMEIARETNFDTGNTYLAIKPGLV 360  
QY 361 IGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 409  
DB 361 IGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 409

RESULT 5  
US-10-674-666-7  
; Sequence 7, Application US/10674666  
; Publication No. US20040131604A1  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Mike A.  
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo  
; FILE REFERENCE: PHOS0001-100  
; CURRENT APPLICATION NUMBER: US/10/674,666  
; CURRENT FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: US 60/427,497  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Mycoplasma arthritidis  
US-10-674-666-7

Query Match 84.8%; Score 1797.5; DB 16; Length 409;  
Best Local Similarity 84.4%; Pred. No. 2.2e-156;  
Matches 345; Conservative 29; Mismatches 34; Indels 1; Gaps 1;  
QY 1 MSVFDKFNKGIHYVSEIGLETVLHVEPGREIDYITPARLDELLFSAILESHDARKEHQS 60  
DB 1 MSVFDKFNKGIHYVSEIGLETVLHVEPGREIDYITPARLDELLFSAILESHDARKEHQS 60  
QY 61 FVKIMKDRGINVVELTDLVAETVDLASKAAKEBFIEFTLEETVPVLTTEANKKAVRAFLLS 120  
DB 61 FVKIMKDRGINVVELTDLVAETVDLASKAAKEBFIEFTLEETVPVLTTEANKKAVRAFLLS 120  
QY 121 KPT-HEMVFEFMSGITYELGVSENEELIVDPMNLYFTRDPPASVGVNGVTIHFMRVYVR 179  
DB 121 KTSRKLVELMAGITKYDLGVSEADHELIVDPMNLYFTRDPPASVGVNGVTIHFMRVYVR 180  
QY 180 RRETLPARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVVSERTDLDITILL 239  
DB 181 RRETLPARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVVSERTDLDITILL 240  
QY 240 LAKNIKANKEVEFKRIVAINVVKWNTNLMHLDITWLTMDKNKFLYSPANDVFKFWDYDLV 299  
DB 241 LAKNLVANKECFKRIIVAINVVKWNTNLMHLDITWLTMDKNKFLYSPANDVFKFWDYDLV 300

QY 300 NGGAEPQOLNGLPLDKLASIINKEPVLPIPGGAGATEMEIARETNFDTGNTYLAIKPGL 359  
DB 301 NGGAEPQOLNGLPLDKLASIINKEPVLPIPGGAGATEMEIARETNFDTGNTYLAIRPGV 360  
QY 360 VTGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 408  
DB 361 VTGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 409  
RESULT 6  
US-10-674-666-9  
; Sequence 9, Application US/10674666  
; Publication No. US20040131604A1  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Mike A.  
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo  
; FILE REFERENCE: PHOS0001-100  
; CURRENT APPLICATION NUMBER: US/10/674,666  
; CURRENT FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: US 60/427,497  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Mycoplasma arthritidis  
US-10-674-666-9

Query Match 84.6%; Score 1793.5; DB 16; Length 409;  
Best Local Similarity 84.1%; Pred. No. 5.2e-156;  
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;  
QY 1 MSVFDKFNKGIHYVSEIGLETVLHVEPGREIDYITPARLDELLFSAILESHDARKEHQS 60  
DB 1 MSVFDKFNKGIHYVSEIGLETVLHVEPGREIDYITPARLDELLFSAILESHDARKEHQS 60  
QY 61 FVKIMKDRGINVVELTDLVAETVDLASKAAKEBFIEFTLEETVPVLTTEANKKAVRAFLLS 120  
DB 61 FVKIMKDRGINVVELTDLVAETVDLASKAAKEBFIEFTLEETVPVLTTEANKKAVRAFLLS 120  
QY 121 KPT-HEMVFEFMSGITYELGVSENEELIVDPMNLYFTRDPPASVGVNGVTIHFMRVYVR 179  
DB 121 KTSRKLVELMAGITKYDLGVSEADHELIVDPMNLYFTRDPPASVGVNGVTIHFMRVYVR 180  
QY 180 RRETLPARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVVSERTDLDITILL 239  
DB 181 RRETLPARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVVSERTDLDITILL 240  
QY 240 LAKNIKANKEVEFKRIVAINVVKWNTNLMHLDITWLTMDKNKFLYSPANDVFKFWDYDLV 299  
DB 241 LAKNLVANKECFKRIIVAINVVKWNTNLMHLDITWLTMDKNKFLYSPANDVFKFWDYDLV 300  
QY 300 NGGAEPQOLNGLPLDKLASIINKEPVLPIPGGAGATEMEIARETNFDTGNTYLAIKPGL 359  
DB 301 NGGAEPQOLNGLPLDKLASIINKEPVLPIPGGAGATEMEIARETNFDTGNTYLAIRPGV 360  
QY 360 VTGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 408  
DB 361 VTGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 409

RESULT 7  
US-10-674-666-10  
; Sequence 10, Application US/10674666  
; Publication No. US20040131604A1  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Mike A.  
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo  
; FILE REFERENCE: PHOS0001-100  
; CURRENT APPLICATION NUMBER: US/10/674,666  
; CURRENT FILING DATE: 2003-09-29

		PRIORITY APPLICATION NUMBER: US 60/427,497	
		PRIOR FILING DATE: 2002-11-18	
		NUMBER OF SEQ ID NOS: 21	
		SOFTWARE: Patent in version 3.2	
		SEQ ID NO 10	
		LENGTH: 409	
		TYPE: PRT	
		ORGANISM: Mycoplasma arthritidis	
		US-10-674-666-10	
		Query Match 84.6%; Score 1793.5; DB 16; Length 409;	
		Best Local Similarity 84.8%; Pred. No. 5.2e-156;	
		Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;	
Qy	1	MSVDSKFGNGIHVYSEIGELETVLVHEPGREIDYITPARLDELFSAILSHDARKEHQS	60
Db	1	MSVDSKFGNGIHVYSEIGELESVLVHEPGREIDYITPARLDELFSAILSHDARKEQS	60
Qy	61	FVKIMKDRGINNVVELTDLVAETDYLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLS	120
Db	61	FVAILKANDINVVETDILVAETDYLASQEAQRLEIEFLEDESEPVLSAHESVVRNFKLA	120
Qy	121	KPT-HEMVPEFMSGITKYELGVSENELIVDPMNLYFTRDPPASVGVNGVTIHFMYIYR	179
Db	121	KTSRKLVELMAGITKYDLGVADHDLIVDPMNLYFTRDPPASVGVNGVTIHFMYIYR	180
Qy	180	RETELFAFVRFRNHPKLVNTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLDITL	239
Db	181	RRETLFSRFRVFNHPKLVNTPWYDPAKMLISIEGSDVFIYNNETLVVGVSERTDLDITL	240
Qy	240	LAKNIKANKEVEFKRIVAINVVKWTNLMHLDITLWMLDKNKFYSPIANDVFKFWDYDLV	299
Db	241	LAKNLVANKECEFKRIVAINVVKWTNLMHLDITLWMLDKNKFYSPIANDVFKFWDYDLV	300
Qy	300	NGAEPQOLNGLPDLKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGTNYLAIKPG	359
Db	301	NGAEPQPVENGLPLEKLLQSIINKPVLIPAGEGASQMEIERETHFDGTNYLAIKPG	360
Qy	360	VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK	408
Db	361	VIGYSRNEKTNAAKAAAGIKVLFPFHGNQLSLGMGNARCMSPLSRKDVK	409
RESULT 9			
US-10-674-666-5			
Sequence 5, Application US/10674666			
Publication No. US20040131604A1			
GENERAL INFORMATION:			
APPLICANT: Clark, Mike A.			
TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo			
FILE REFERENCE: PHO0001-100			
CURRENT APPLICATION NUMBER: US/10/674,666			
CURRENT FILING DATE: 2003-09-29			
PRIOR APPLICATION NUMBER: US 60/427,497			
PRIOR FILING DATE: 2002-11-18			
NUMBER OF SEQ ID NOS: 21			
SOFTWARE: Patent in version 3.2			
SEQ ID NO 5			
LENGTH: 410			
TYPE: PRT			
ORGANISM: Mycoplasma arginini			
US-10-674-666-5			
		Query Match 83.2%; Score 1764.5; DB 16; Length 410;	
		Best Local Similarity 82.0%; Pred. No. 2.4e-153;	
		Matches 336; Conservative 37; Mismatches 36; Indels 1; Gaps 1;	
Qy	1	MSVDSKFGNGIHVYSEIGELETVLVHEPGREIDYITPARLDELFSAILSHDARKEHQS	60
Db	1	MSVDSKFGNGIHVYSEIGELESVLVHEPGREIDYITPARLDELFSAILSHDARKEHQ	60
Qy	61	FVKIMKDRGINNVVELTDLVAETDYLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLS	120
Db	61	FVAILKANDINVVETDILVAETDYLASQEAQRLEIEFLEDESEPVLSAHESVVRNFKLA	120
Qy	121	KPT-HEMVPEFMSGITKYELGVSENELIVDPMNLYFTRDPPASVGVNGVTIHFMYIYR	179
Db	121	KTSRKLVELMAGITKYDLGVADHDLIVDPMNLYFTRDPPASVGVNGVTIHFMYIYR	180
Qy	180	RETELFAFVRFRNHPKLVNTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLDITL	239
Db	181	RRETLFSRFRVFNHPKLVNTPWYDPAKMLISIEGSDVFIYNNETLVVGVSERTDLDITL	240
Qy	240	LAKNIKANKEVEFKRIVAINVVKWTNLMHLDITLWMLDKNKFYSPIANDVFKFWDYDLV	299
Db	241	LAKNLVANKECEFKRIVAINVVKWTNLMHLDITLWMLDKNKFYSPIANDVFKFWDYDLV	300
Qy	300	NGAEPQOLNGLPDLKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGTNYLAIKPG	359
Db	301	NGAEPQPVENGLPLEKLLQSIINKPVLIPAGEGASQMEIERETHFDGTNYLAIKPG	360
Qy	360	VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK	408
RESULT 8			
US-10-674-666-8			
Sequence 8, Application US/10674666			
Publication No. US20040131604A1			
GENERAL INFORMATION:			
APPLICANT: Clark, Mike A.			
TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo			
FILE REFERENCE: PHO0001-100			
CURRENT APPLICATION NUMBER: US/10/674,666			
CURRENT FILING DATE: 2003-09-29			
PRIOR APPLICATION NUMBER: US 60/427,497			
PRIOR FILING DATE: 2002-11-18			
NUMBER OF SEQ ID NOS: 21			
SOFTWARE: Patent in version 3.2			
SEQ ID NO 8			
LENGTH: 409			
TYPE: PRT			
ORGANISM: Mycoplasma arthritidis			
US-10-674-666-8			
		Query Match 84.4%; Score 1789.5; DB 16; Length 409;	
		Best Local Similarity 83.9%; Pred. No. 1.2e-155;	
		Matches 343; Conservative 31; Mismatches 34; Indels 1; Gaps 1;	
Qy	1	MSVDSKFGNGIHVYSEIGELETVLVHEPGREIDYITPARLDELFSAILSHDARKEHQS	60
Db	1	MSVDSKFGNGIHVYSEIGELESVLVHEPGREIDYITPARLDELFSAILSHDARKEQS	60
Qy	61	FVKIMKDRGINNVVELTDLVAETDYLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLS	120

Db 361 VIGYSRNEKTXAALAAAGIKVLPFHGNQLSLGNGNARCMPLSRKDKVKW 410

RESULT 10

US-10-343-175-10

Sequence 10, Application US/10343175

Best Local Similarity 82.0%; Pred. No. 3e-153;

Publication No. US20040096437A1

GENERAL INFORMATION:

APPLICANT: Angiolab, Inc.

TITLE OF INVENTION: The pharmaceutical composition containing arginine deiminase for inhibiting angiogenesis

FILE REFERENCE: PCA/KR01/01281

CURRENT APPLICATION NUMBER: US/10/343,175

CURRENT FILING DATE: 2003-01-24

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Kopatentin 1.71

SEQ ID NO 10

LENGTH: 410

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Amino acids coding Mycoplasma Arginine Deiminase

US-10-343-175-10

Query Match 83.2%; Score 1763.5; DB 15; Length 410;

Best Local Similarity 82.0%; Pred. No. 3e-153;

Matches 336; Conservative 37; Mismatches 36; Indels 1; Gaps 1;

QY 1 MSVFSKFGNGIHVYSEIGLETVLVHEPGREIDYITPARLDELLFSAILES HDARKEHQS 60

Db 1 MSVFSKFGNGIHVYSEIGLESVLVHEPGREIDYITPARLDELLFSAILES HDARKEHQ 60

QY 61 FVKIMKDRGINVVELTDLVAETDYDLASKAAKEEFIEETLEETVPVLTEANKKAVRAFLLS 120

Db 61 FVAELKANDINVVELLDVAETDYDLASQAKOKLIEEFLEDEPVLSESHKVVVRNFLKA 120

QY 121 KPT-HEMVEFMMSGITKYELGVSENELIVDMPNLYFTRDPFASVGVNGVTIHFMYIYVR 179

Db 121 KTSRELVEIMMAGITKYDLGIEADHELIVDMPNLYFTRDPFASVGVNGVTIHYMYKYR 180

QY 180 RRETLPARFVRNHPKLVKTPWYDPAKMPLEGGDVFTYNNETLVVGVSRERDLDITTL 239

Db 181 QRETLFSRFVSNHPKLINTPWYDPSLKSLIEGGDVFTYNNETLVVGVSRERDLDITTL 240

QY 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKDKFLYSPFIANDVPKFWDYDLV 299

Db 241 LAKSIVANKECFKRIIVAINVPKWTNLMHLDTWLMDKDKFLYSPFIANDVPKFWDYDLV 300

QY 300 NGGABPQPOLNGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGL 359

Db 301 NGGABPQPVENGPLEGLLQSIINKKPVLIPIAGEGASQMEIERETHFDGTNYLAIRPGV 360

QY 360 VTGYDRNEKTXAALAAAGITVLPFHGNQLSLGNGNARCMPLSRKDKVKW 409

Db 361 VIGYSRNEKTXAALAAAGIKVLPFHGNQLSLGNGNARCMPLSRKDKVKW 410

RESULT 11

US-10-674-666-6

Sequence 6, Application US/10674666

Best Local Similarity 82.0%; Pred. No. 3e-153;

Publication No. US20040131604A1

GENERAL INFORMATION:

APPLICANT: Clark, Mike A.

TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo

FILE REFERENCE: PHOS001-100

CURRENT APPLICATION NUMBER: US/10/674,666

CURRENT FILING DATE: 2003-09-29

NUMBER OF SEQ ID NOS: 21

SOFTWARE: Patent in version 3.2

SEQ ID NO 6

LENGTH: 410

TYPE: PRT

ORGANISM: Mycoplasma arginini

US-10-674-666-6

Query Match 83.0%; Score 1760.5; DB 16; Length 410;

Best Local Similarity 81.7%; Pred. No. 5.7e-153;

Matches 335; Conservative 38; Mismatches 36; Indels 1; Gaps 1;

QY 1 MSVFSKFGNGIHVYSEIGLETVLVHEPGREIDYITPARLDELLFSAILES HDARKEHQS 60

Db 1 MSVFSKFGNGIHVYSEIGLESVLVHEPGREIDYITPARLDELLFSAILES HDARKEHQ 60

QY 61 FVKIMKDRGINVVELTDLVAETDYDLASKAAKEEFIEETLEETVPVLTEANKKAVRAFLLS 120

Db 61 FVAELKANDINVVELLDVAETDYDLASQAKOKLIEEFLEDEPVLSESHKVVVRNFLKA 120

QY 121 KPT-HEMVEFMMSGITKYELGVSENELIVDMPNLYFTRDPFASVGVNGVTIHFMYIYVR 179

Db 121 KTSRELVEIMMAGITKYDLGIEADHELIVDMPNLYFTRDPFASVGVNGVTIHYMYKYR 180

QY 180 RRETLPARFVRNHPKLVKTPWYDPAKMPLEGGDVFTYNNETLVVGVSRERDLDITTL 239

Db 181 QRETLFSRFVSNHPKLINTPWYDPSLKSLIEGGDVFTYNNETLVVGVSRERDLDITTL 240

QY 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKDKFLYSPFIANDVPKFWDYDLV 299

Db 241 LAKNIVANKECFKRIIVAINVPKWTNLMHLDTWLMDKDKFLYSPFIANDVPKFWDYDLV 300

QY 300 NGGABPQPOLNGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGL 359

Db 301 NGGABPQPVENGPLEGLLQSIINKKPVLIPIAGEGASQMEIERETHFDGTNYLAIRPGV 360

QY 360 VTGYDRNEKTXAALAAAGITVLPFHGNQLSLGNGNARCMPLSRKDKVKW 409

Db 361 VIGYSRNEKTXAALAAAGIKVLPFHGNQLSLGNGNARCMPLSRKDKVKW 410

RESULT 12

US-10-369-493-16696

Sequence 16696, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 16696

LENGTH: 410

TYPE: PRT

ORGANISM: Bacillus thuringiensis

US-10-369-493-16696

Query Match 33.4%; Score 707.5; DB 14; Length 410;

Best Local Similarity 40.9%; Pred. No. 3.9e-56;

Matches 169; Conservative 70; Mismatches 151; Indels 23; Gaps 10;

QY 11 IHVYSEIGLETVLVHEPGREIDYITPARLDELLFSAILES HDARKEHQS FVKIMKDRGI 70

Db 5 IHVTSIGELQIVLVKRGKEVENLTPDYQLQLLFDIDIPYLPQIKEDHYFAQTLANRGV 64

QY 71 NVVELTDLVAETDYDLASKAAKEEFIEETLEETVPVLTEANKKAVRAFLLSKPHVWEPF 130

Db 65 EVLYLEKAAEA--LVDDKKLREBEFVDRIKQEGADVNVVAH-QTLKEYLLSFSNEELIQKI 121

```
QY 131 MSGITK-----YELGVSENELIYDPMENLYFTRDPFASVGNVTHIFMYIVR 179
Db 122 MGVRKNEIETSKTHLYEL-MEDHYFFYLDPMENLYFTRDPFASVGDGLTIKMKREPAR 180
QY 180 RRETFLARFVRNHPKLVK--TPWYDPAKMPFIEGGDVFIYNNETLVVGVSERTDLDTI 237
Db 181 RRESLFMEYIIKYHPRFAKHNPVILWDRDYKFFIEGGDELILNEETIAIGVSARTSAKAI 240
QY 238 TLLAKNTKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSP-IANDVFKFWY 296
Db 241 ERLAKNL-FSQNKIKKVLAEIPKCRFAFWHLDTVFTMVVDYDKFTIHPAIGQKGNMNIY 299
QY 297 DLVNGGAEPQOL-NGPLDKLASIIN-KEPVLPIPGGAGATEMETARETNFDGNTYLA 354
Db 300 ILEKGSDEELTKTHRTSLMEALKEVGLSELVLI PCGGDV--IASAREQWNDGNTLA 357
QY 355 IKPGLVIGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDV 407
Db 358 IAPGVVVYDRNVVSNLTLLREHGIEVIEVLSSLSRGRGPRCWMPIVRKDI 410

RESULT 13
US-10-674-666-19
; Sequence 19, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; PRIOR FILING DATE: 2003-09-29
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 19
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-674-666-19

Query Match 32.1%; Score 681.5; DB 16; Length 413;
Best Local Similarity 38.4%; Pred. No. 9.6e-54;
Matches 163; Conservative 66; Mismatches 152; Indels 43; Gaps 7;

QY 11 IHVYSIGELETVLVHEPGREIDYITPARLDELLFSAILESHPDARKEHQSFKVIMKDRGI 70
Db 7 IHVYSIGPLKTYMLKRPGRLENLTPEYLERLLFDDIPFLPAVQKEHQFAETLKQOGA 66
QY 71 NVVELTDLVAETVDLASKAAKEEFITFLEETVPVLTEANKKAVRAFLLSKPTHEMVFEF 130
Db 67 EVLYLEKLTAEALDDA--LVREQIDELLETESKADINGAYDR-LKEFLLTFDADSWEQV 123
QY 131 MSGITKYELGVSENEL-----IVDPMENLYFTRDPFASVGNVTHIFMYIVR 180
Db 124 MSGIRKNELEREKXSHLHELMEDHYPPYLDPMENLYFTRDPFAAAGSLTINKMKEPARR 183
QY 181 RETFLARFVRNHPKLV--KTPWYDPAKMPFIEGGDVFIYNNETLVVGVSERTDLDTIT 238
Db 184 RESLFMYIINHPRFKGHIPEIPLWDRDFKNIEGGDELVLNEETVAIGVSERTTAQAE 243
QY 239 LLAKNITKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSP-IANDVFKFWYDL 298
Db 244 RLVRNL-FQQRIRRVLAIVEIPKSAFWHLDTVFTMVDRDQFTIHPAQ-----292
QY 299 VNGGAEPPQNLGLPDKLASIINKEPVLIP-----IGGAGATEMIARE 344
Db 293 ---GPEGDMRIFVLERGKTADEIHTTEHNHLPVLRKTLGLSDWNLIFCGGGEIASARE 349
QY 345 TNPDGNTYLAIKPGLVIGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSR 404
Db 350 QWNDGNTLAIPGVVVYDRNVYISNRECUQGIKVIETPSGELSRGRGPRCWMSPLYR 409
```

```
QY 405 KDVK 408
Db 410 EDVK 413

RESULT 14
US-10-674-666-13
; Sequence 13, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; PRIOR FILING DATE: 2003-09-29
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 13
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-674-666-13

Query Match 32.0%; Score 679; DB 16; Length 411;
Best Local Similarity 39.4%; Pred. No. 1.6e-53;
Matches 163; Conservative 70; Mismatches 155; Indels 26; Gaps 10;

QY 11 IHVYSIGELETVLVHEPGREIDYITPARLDELLFSAILESHPDARKEHQSFKVIMKDRGI 70
Db 7 IHVYSIGKLKKVLLHRPKGEIENLMPDYLERLLFDDIPFLDAQKEHDAFAQALRDEGI 66
QY 71 NVVELTDLVAETVDLASKAAKEEFITFLEETVPVLTEANKKAVRAFLLS-KPTHEMVFEF 129
Db 67 EVLYLETLAAES--LVTPEIREAFIDEVLYSE-ANIRGRATKKAIRELLMAIEDNQELIEK 123
QY 130 MMSGITKYELG-----VSENELIYDPMENLYFTRDPFASVGNVTHIFMYI 177
Db 124 TWAGVQKSELPEIPASEKGLTDLVESNYPFADPMENLYFTRDPFATIGVSLNHMFSE 183
QY 178 VRRRETFLARFVRNHPKLV--VKTPWYDPAKMPFIEGGDVFIYNNETLVVGVSERTDL 235
Db 184 TRNRETLYCKYIFTHPIYGGKVPWYDRNETTRIEGGDELVLKDLAVGLSQRDAA 243
QY 236 TITLAKNTKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSP-IANDVFKFW 294
Db 244 SIEKLLVNI-FKQNLGFKVLAFEFANNRKFWEHLDVFTMVVDYDKFTIHPTEIGDLRV-- 300
QY 295 DYDLVNGGAEPQQLNGLPLDKLASIINKEPVL-LIPIGGAGATEMEIARETNFDGNTYL 353
Db 301 -XSVTYDNEELHIVEEKGLAEALLANLGVKVDLIRCGDNL--VAAGREQWNDGNTL 357
QY 354 AIKPGLVIGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDV 407
Db 358 TIAPGVVVVYNNRTIINALESKGLKLIKHGSELVRGRGPRCWMSPFEREDI 411

RESULT 15
US-10-674-666-20
; Sequence 20, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; CURRENT FILING DATE: 2003-09-29
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 20
```



THIS PAGE BLANK (USPTO)



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2004, 15:44:59 ; Search time 39 seconds  
(without alignments)  
695.489 Million cell updates/sec

Title: US-10-674-666-1

Perfect score: 2120

Sequence: 1 MSVFDKFGNGIHVYSEIGLE.....LGMGNARCMPLSRKDKVKW 409

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PCRUS COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2120	100.0	409	3	US-09-023-809B-3
2	2120	100.0	409	4	US-09-564-559B-1
3	2120	100.0	409	4	US-09-723-546-3
4	2116	99.8	409	4	US-09-564-559B-2
5	2112	99.6	409	4	US-09-564-559B-3
6	2108	99.4	409	4	US-09-564-559B-4
7	2098.5	99.0	410	1	US-08-792-283A-8
8	2098.5	99.0	410	2	US-09-105-908-8
9	2098.5	99.0	410	3	US-09-271-713-8
10	1807.5	85.3	410	3	US-09-023-809B-2
11	1807.5	85.3	410	4	US-09-723-546-2
12	1793.5	84.6	409	4	US-09-564-559B-7
13	1789.5	84.4	409	4	US-09-564-559B-9
14	1789.5	84.4	409	4	US-09-564-559B-10
15	1785.5	84.2	409	4	US-09-564-559B-8
16	1765.5	83.3	410	1	US-08-792-283A-7
17	1765.5	83.3	410	2	US-09-105-908-7
18	1765.5	83.3	410	3	US-09-271-713-7
19	1764.5	83.2	410	3	US-09-023-809B-1
20	1764.5	83.2	410	4	US-09-723-546-1
21	1746.5	82.4	409	4	US-09-564-559B-5
22	1742.5	82.2	409	4	US-09-564-559B-6
23	1732.5	81.7	410	1	US-08-792-283A-2
24	1732.5	81.7	410	2	US-09-105-908-2
25	1732.5	81.7	410	3	US-09-271-713-2
26	1713.5	80.8	410	1	US-08-792-283A-9
27	1713.5	80.8	410	2	US-09-105-908-9

28	1713.5	80.8	410	3	US-09-271-713-9	Sequence 9, Appli
29	1698.5	80.1	399	6	5474928-2	Patent No. 5474928
30	681.5	32.1	413	4	US-09-723-546-12	Sequence 12, Appl
31	679	32.0	411	4	US-09-723-546-6	Sequence 6, Appli
32	670.5	31.6	408	4	US-09-723-546-13	Sequence 13, Appl
33	667.5	31.5	417	4	US-09-107-532A-6148	Sequence 6148, Ap
34	655	30.9	413	4	US-09-723-546-11	Sequence 11, Appl
35	652.5	30.8	409	4	US-09-583-110-4274	Sequence 4274, Ap
36	651.5	30.7	409	4	US-09-723-546-7	Sequence 7, Appli
37	640.5	30.2	411	3	US-08-964-652-2	Sequence 2, Appli
38	640.5	30.2	422	3	US-09-134-001C-2931	Sequence 2931, Ap
39	625	29.5	409	4	US-09-723-546-14	Sequence 14, Appl
40	618	29.2	420	3	US-09-134-001C-4427	Sequence 4427, Ap
41	612.5	28.9	410	4	US-09-723-546-8	Sequence 8, Appli
42	604.5	28.5	394	4	US-09-710-279-58	Sequence 58, Appl
43	600.5	28.3	409	4	US-09-723-546-9	Sequence 9, Appli
44	581.5	27.4	379	4	US-09-134-000C-6027	Sequence 6027, Ap
45	474	22.4	356	4	US-09-710-279-2488	Sequence 2488, Ap

ALIGNMENTS

RESULT 1  
US-09-023-809B-3  
; Sequence 3, Application US/09023809B  
; Patent No. 6183738  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Mike A  
; TITLE OF INVENTION: Modified Arginine Deiminase  
; FILE REFERENCE: PHOE0028  
; CURRENT APPLICATION NUMBER: US/09/023,809B  
; CURRENT FILING DATE: 2000-02-13  
; PRIOR APPLICATION NUMBER: 60/046,200  
; PRIOR FILING DATE: 1997-05-12  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Mycoplasma hominis  
; US-09-023-809B-3

Query Match	100.0%	Score 2120;	DB 3;	Length 409;
Best Local Similarity	100.0%	Pred. No. 1.9e-212;		
Matches 409;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MSVFDKFGNGIHVYSEIGLETVLVHVEPGREIDYITPARLDELLFSAILES HDARKEHQ	60	
Db	1	MSVFDKFGNGIHVYSEIGLETVLVHVEPGREIDYITPARLDELLFSAILES HDARKEHQ	60	
QY	61	FKIMKDRGINVVELTDLVAETVDLASKAAKEEFITFLEETVPVLTEANKKAVRAFLS	120	
Db	61	FKIMKDRGINVVELTDLVAETVDLASKAAKEEFITFLEETVPVLTEANKKAVRAFLS	120	
QY	121	KPTHEWVEFMGSGITKYLGVSENELIVDPMNLFTDRDPPASVGVGVTIHPMRYVRR	180	
Db	121	KPTHEWVEFMGSGITKYLGVSENELIVDPMNLFTDRDPPASVGVGVTIHPMRYVRR	180	
QY	181	RETLPARFVRNHPKLVKTPWYYDPAMKMPIEGGDVFIYNNETLVVGVSERTDLTITLL	240	
Db	181	RETLPARFVRNHPKLVKTPWYYDPAMKMPIEGGDVFIYNNETLVVGVSERTDLTITLL	240	
QY	241	AKNIKANKEVEFKRIIVAINVPKWTNLMHLDLTMLDKKFLYSPIANDVFKFWDVLVN	300	
Db	241	AKNIKANKEVEFKRIIVAINVPKWTNLMHLDLTMLDKKFLYSPIANDVFKFWDVLVN	300	
QY	301	GGAEPOQLNGPLDKLLASINKEPVLPIGGAGATEMEIARETNFDGNTYLAIKPLV	360	
Db	301	GGAEPOQLNGPLDKLLASINKEPVLPIGGAGATEMEIARETNFDGNTYLAIKPLV	360	
QY	361	IGYDRNEKTNAAKAGITVLPFHGNQLSIMGNARCMPLSRKDKVKW	409	
Db	361	IGYDRNEKTNAAKAGITVLPFHGNQLSIMGNARCMPLSRKDKVKW	409	

```
Db      361 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominis
US-09-723-546-3

Query Match      100.0%; Score 2120; DB 4; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.9e-212;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MSVFDSKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60
DB      1 MSVFDSKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60
QY      61 FVKIMKDRGINNVVELTDLVAETDYDLASKAAKEEFIEFTFLEETVPVLTTEANKKAVRAFLLS 120
DB      61 FVKIMKDRGINNVVELTDLVAETDYDLASKAAKEEFIEFTFLEETVPVLTTEANKKAVRAFLLS 120
QY      121 KPTHEMVFEFMMSGITKYELGVSENELIVDPMNLYFTRDPPASVGVNGVTIHFMRIVRR 180
DB      121 KPTHEMVFEFMMSGITKYELGVSENELIVDPMNLYFTRDPPASVGVNGVTIHFMRIVRR 180
QY      181 RETLFARFVRNHPKLVKTPWYDDPAMKMPIEGGDVFIYNNETLVVGVSERTDLDITLL 240
DB      181 RETLFARFVRNHPKLVKTPWYDDPAMKMPIEGGDVFIYNNETLVVGVSERTDLDITLL 240
QY      241 AKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFYSPIANDVFKFWDYDLVN 300
DB      241 AKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFYSPIANDVFKFWDYDLVN 300
QY      301 GGAEPQPOLNGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGLV 360
DB      301 GGAEPQPOLNGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGLV 360
QY      361 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409
DB      361 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409

RESULT 4
US-09-564-559B-2
; Sequence 2, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: PCT/US01/14116
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominis
US-09-564-559B-2

Query Match      99.8%; Score 2116; DB 4; Length 409;
Best Local Similarity 99.8%; Pred. No. 4.9e-212;
Matches 408; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MSVFDSKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60
DB      1 MSVFDSKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60
QY      61 FVKIMKDRGINNVVELTDLVAETDYDLASKAAKEEFIEFTFLEETVPVLTTEANKKAVRAFLLS 120
DB      61 FVKIMKDRGINNVVELTDLVAETDYDLASKAAKEEFIEFTFLEETVPVLTTEANKKAVRAFLLS 120
QY      121 KPTHEMVFEFMMSGITKYELGVSENELIVDPMNLYFTRDPPASVGVNGVTIHFMRIVRR 180
DB      121 KPTHEMVFEFMMSGITKYELGVSENELIVDPMNLYFTRDPPASVGVNGVTIHFMRIVRR 180
QY      181 RETLFARFVRNHPKLVKTPWYDDPAMKMPIEGGDVFIYNNETLVVGVSERTDLDITLL 240
DB      181 RETLFARFVRNHPKLVKTPWYDDPAMKMPIEGGDVFIYNNETLVVGVSERTDLDITLL 240
QY      241 AKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFYSPIANDVFKFWDYDLVN 300
DB      241 AKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFYSPIANDVFKFWDYDLVN 300
QY      301 GGAEPQPOLNGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGLV 360
DB      301 GGAEPQPOLNGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGLV 360
QY      361 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409
DB      361 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409

RESULT 3
US-09-723-546-3
; Sequence 3, Application US/09723546
; Patent No. 6737259
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A
; TITLE OF INVENTION: Modified Arginine Deiminase
; FILE REFERENCE: PHOE0059
; CURRENT APPLICATION NUMBER: US/09/723,546
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/023,809
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 14
```

Db 61 FVKIMKDRGINVVELTDLVAETVYDLASKAAKEFIETFLSETPVLTPEANKEAVRAFLLS 120  
QY 121 KPHEMVEFWMGSIITKYELGVSENELIVDPMPNLVETPRDPFASVGNVGTIHFMRVIVRR 180  
Db 121 KPHEMVEFWMGSIITKYELGVSENELIVDPMPNLVETPRDPFASVGNVGTIHFMRVIVRR 180  
QY 181 RETLFAFVRNHPKLVKTPWYDDPAMKPIEGGDVFIYNNETLVVGVSERTDLDITILL 240  
Db 181 RETLFAFVRNHPKLVKTPWYDDPAMKPIEGGDVFIYNNETLVVGVSERTDLDITILL 240  
QY 241 AKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVFKFWDYDLVN 300  
Db 241 AKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVFKFWDYDLVN 300  
QY 301 GGAEPQQLNGLPLDKLLASIIINKEPVLPIGGAGATEMEIARETNPFGDGTNYLAIKPGLV 360  
Db 301 GGAEPQQLNGLPLDKLLASIIINKEPVLPIGGAGATEMEIARETNPFGDGTNYLAIKPGLV 360  
QY 361 IGYDRNEKTNAAKAAAGITVLPFHGNQSLGGMGNARCMSPLSRKDVVK 409  
Db 361 IGYDRNEKTNAAKAAAGITVLPFHGNQSLGGMGNARCMSPLSRKDVVK 409

## RESULT 5

US-09-564-559B-3  
; Sequence 3, Application US/09564559B  
; Patent No. 6635462  
; GENERAL INFORMATION:  
; APPLICANT: Ensor, Charles Mark  
; APPLICANT: Holtberg, Frederick Wayne  
; APPLICANT: Clark, Mike A.  
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase  
; FILE REFERENCE: PHOE0033  
; CURRENT APPLICATION NUMBER: US/09/564,559B  
; CURRENT FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 09/564,559  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR FILING DATE: 2001-05-02  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Mycoplasma hominis  
US-09-564-559B-3

Query Match 99.6%; Score 2112; DB 4; Length 409;  
Best Local Similarity 99.8%; Pred. No. 1.3e-211;  
Matches 408; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MSVFDKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60  
Db 1 MSVFDKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60  
QY 61 FVKIMKDRGINVVELTDLVAETVYDLASKAAKEFIETFLSETPVLTPEANKEAVRAFLLS 120  
Db 61 FVKIMKDRGINVVELTDLVAETVYDLASKAAKEFIETFLSETPVLTPEANKEAVRAFLLS 120  
QY 121 KPHEMVEFWMGSIITKYELGVSENELIVDPMPNLVETPRDPFASVGNVGTIHFMRVIVRR 180  
Db 121 KPHEMVEFWMGSIITKYELGVSENELIVDPMPNLVETPRDPFASVGNVGTIHFMRVIVRR 180  
QY 181 RETLFAFVRNHPKLVKTPWYDDPAMKPIEGGDVFIYNNETLVVGVSERTDLDITILL 240  
Db 181 RETLFAFVRNHPKLVKTPWYDDPAMKPIEGGDVFIYNNETLVVGVSERTDLDITILL 240  
QY 241 AKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVFKFWDYDLVN 300  
Db 241 AKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVFKFWDYDLVN 300  
QY 301 GGAEPQQLNGLPLDKLLASIIINKEPVLPIGGAGATEMEIARETNPFGDGTNYLAIKPGLV 360

Db 301 GGAEPQQLNGLPLDKLLASIIINKEPVLPIGGAGATEMEIARETNPFGDGTNYLAIKPGLV 360  
QY 361 IGYDRNEKTNAAKAAAGITVLPFHGNQSLGGMGNARCMSPLSRKDVVK 409  
Db 361 IGYDRNEKTNAAKAAAGITVLPFHGNQSLGGMGNARCMSPLSRKDVVK 409

## RESULT 6

US-09-564-559B-4  
; Sequence 4, Application US/09564559B  
; Patent No. 6635462  
; GENERAL INFORMATION:  
; APPLICANT: Ensor, Charles Mark  
; APPLICANT: Holtberg, Frederick Wayne  
; APPLICANT: Clark, Mike A.  
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase  
; FILE REFERENCE: PHOE0033  
; CURRENT APPLICATION NUMBER: US/09/564,559B  
; CURRENT FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 09/564,559  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: PCT/US01/14116  
; PRIOR FILING DATE: 2001-05-02  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Mycoplasma hominis  
US-09-564-559B-4

Query Match 99.4%; Score 2108; DB 4; Length 409;  
Best Local Similarity 99.5%; Pred. No. 3.4e-211;  
Matches 407; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MSVFDKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60  
Db 1 MSVFDKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60  
QY 61 FVKIMKDRGINVVELTDLVAETVYDLASKAAKEFIETFLSETPVLTPEANKEAVRAFLLS 120  
Db 61 FVKIMKDRGINVVELTDLVAETVYDLASKAAKEFIETFLSETPVLTPEANKEAVRAFLLS 120  
QY 121 KPHEMVEFWMGSIITKYELGVSENELIVDPMPNLVETPRDPFASVGNVGTIHFMRVIVRR 180  
Db 121 KPHEMVEFWMGSIITKYELGVSENELIVDPMPNLVETPRDPFASVGNVGTIHFMRVIVRR 180  
QY 181 RETLFAFVRNHPKLVKTPWYDDPAMKPIEGGDVFIYNNETLVVGVSERTDLDITILL 240  
Db 181 RETLFAFVRNHPKLVKTPWYDDPAMKPIEGGDVFIYNNETLVVGVSERTDLDITILL 240  
QY 241 AKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVFKFWDYDLVN 300  
Db 241 AKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVFKFWDYDLVN 300  
QY 301 GGAEPQQLNGLPLDKLLASIIINKEPVLPIGGAGATEMEIARETNPFGDGTNYLAIKPGLV 360  
Db 301 GGAEPQQLNGLPLDKLLASIIINKEPVLPIGGAGATEMEIARETNPFGDGTNYLAIKPGLV 360  
QY 361 IGYDRNEKTNAAKAAAGITVLPFHGNQSLGGMGNARCMSPLSRKDVVK 409  
Db 361 IGYDRNEKTNAAKAAAGITVLPFHGNQSLGGMGNARCMSPLSRKDVVK 409

## RESULT 7

US-08-792-283A-8  
; Sequence 8, Application US/08792283A  
; Patent No. 5804183  
; GENERAL INFORMATION:  
; APPLICANT: Filpula, David  
; APPLICANT: Wang, Maoliang  
; TITLE OF INVENTION: Arginine Deiminase Derived From

;; TITLE OF INVENTION: Mycoplasma and Polymer Conjugates Containing the Same  
;; NUMBER OF SEQUENCES: 9  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: ROBERTS & MERCANTI  
;; STREET: 81 Tamarack Circle  
;; CITY: Skillman  
;; STATE: New Jersey  
;; COUNTRY: United States  
;; ZIP: 08558  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA: US/08/792,283A  
;; APPLICATION NUMBER: US/08/792,283A  
;; FILING DATE: 31-JAN-1997  
;; CLASSIFICATION: 428  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mercanti, Michael N.  
;; REGISTRATION NUMBER: 33966  
;; REFERENCE/DOCKET NUMBER: 2131055  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 609-921-3500  
;; TELEFAX: 609-921-9535  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 410 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: NO  
;; ORIGINAL SOURCE:  
;; ORGANISM: Mycoplasma hominis  
;; STRAIN: PG21  
;; CELL TYPE: unicellular  
;;  
US-08-792-283A-8

Query Match 99.0%; Score 2098.5; DB 1; Length 410;  
Best Local Similarity 99.3%; Pred. No. 3.3e-210;  
Matches 407; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
  
Qy 1 MSVDSKFNHGVSEIGLETVLVHPEGRIDYITPARDELLEFSAILESHDARKHQ 60  
Db |||||  
  
Qy 61 FVKIMKDRGINNVVELTDVAETDYLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLS 120  
Db |||||  
  
Qy 121 -KPTHEMVEFPMMSGITKYELGVSENELIVDPMPNLYFTDRDPFASVGVNGVTIHPMRYIVR 179  
Db |||||  
  
Qy 121 QKPTHEMVEFPMMSGITKYELGVSENELIVDPMPNLYFTDRDPFASVGVNGVTIHPMRYIVR 180  
Db |||||  
  
Qy 180 RRETLEFARFVRNHPKLVKTPWYDPAKMPLEGDVFYINNETLVVGVSERTDLDITL 239  
Db |||||  
  
Qy 181 RRETLEFARFVRNHPKLVKTPWYDPAKMPLEGDVFYINNETLVVGVSERTDLDITL 240  
Db |||||  
  
Qy 240 LAKNIKANKEVEFKRIIVAINVPKWTNLMHLDITLMDKKNKFLYSPIANDVFKFWDYDLV 299  
Db |||||  
  
Qy 241 LAKNIKANKEVEFKRIIVAINVPKWTNLMHLDITLMDKKNKFLYSPIANDVFKFWDYDLV 300  
Db |||||  
  
Qy 300 NGGAEPQVLNGLPLDKLLASIIKNEPVLPIGAGATAMEIARETNFDGTNYLAIKPGL 359  
Db |||||  
  
Qy 301 NGGAEPQVLNGLPLDKLLASIIKNEPVLPIGAGATAMEIARETNFDGTNYLAIKPGL 360  
Db |||||  
  
Qy 360 VIGYDRNEKTNAAKAGITVLPFHGNQLSIGMGNARCMSPLSRKDKVK 409  
Db |||||  
  
Qy 361 VIGYDRNEKTNAAKAGITVLPFHGNQLSIGMGNARCMSPLSRKDKVK 410  
Db |||||

US-09-105-908-8  
;; Sequence 8, Application US/09105908  
;; Patent No. 5916793  
;; GENERAL INFORMATION:  
;; APPLICANT: Filpula, David  
;; APPLICANT: Wang, Maoliang  
;; TITLE OF INVENTION: Arginine Deiminase Derived From  
;; TITLE OF INVENTION: Mycoplasma and Polymer Conjugates Containing the Same  
;; NUMBER OF SEQUENCES: 9  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: ROBERTS & MERCANTI  
;; STREET: 81 Tamarack Circle  
;; CITY: Skillman  
;; STATE: New Jersey  
;; COUNTRY: United States  
;; ZIP: 08558  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA: US/09/105,908  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA: US/08/792,283  
;; APPLICATION NUMBER: US/08/792,283  
;; FILING DATE: 31-JAN-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mercanti, Michael N.  
;; REGISTRATION NUMBER: 33966  
;; REFERENCE/DOCKET NUMBER: 2131055  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 609-921-3500  
;; TELEFAX: 609-921-9535  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 410 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: No. 5916793 Relevant  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: NO  
;; ORIGINAL SOURCE:  
;; ORGANISM: Mycoplasma hominis  
;; STRAIN: PG21  
;; CELL TYPE: unicellular  
;;  
US-09-105-908-8

Query Match 99.0%; Score 2098.5; DB 2; Length 410;  
Best Local Similarity 99.3%; Pred. No. 3.3e-210;  
Matches 407; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
  
Qy 1 MSVDSKFNHGVSEIGLETVLVHPEGRIDYITPARDELLEFSAILESHDARKHQ 60  
Db |||||  
  
Qy 61 FVKIMKDRGINNVVELTDVAETDYLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLS 120  
Db |||||  
  
Qy 61 FVKIMKDRGINNVVELTDVAETDYLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLS 120  
Db |||||  
  
Qy 121 -KPTHEMVEFPMMSGITKYELGVSENELIVDPMPNLYFTDRDPFASVGVNGVTIHPMRYIVR 179  
Db |||||  
  
Qy 121 QKPTHEMVEFPMMSGITKYELGVSENELIVDPMPNLYFTDRDPFASVGVNGVTIHPMRYIVR 180  
Db |||||  
  
Qy 180 RRETLEFARFVRNHPKLVKTPWYDPAKMPLEGDVFYINNETLVVGVSERTDLDITL 239  
Db |||||  
  
Qy 181 RRETLEFARFVRNHPKLVKTPWYDPAKMPLEGDVFYINNETLVVGVSERTDLDITL 240  
Db |||||  
  
Qy 240 LAKNIKANKEVEFKRIIVAINVPKWTNLMHLDITLMDKKNKFLYSPIANDVFKFWDYDLV 299  
Db |||||  
  
Qy 241 LAKNIKANKEVEFKRIIVAINVPKWTNLMHLDITLMDKKNKFLYSPIANDVFKFWDYDLV 300  
Db |||||

Qy	300	NGGAEPQPOLNGLPLDKLLASINKEPVLIPIGAGATGEMEIARETNP	359
Db	301	NGGAEPQVLNGLPLDKLLASINKEPVLIPIGAGATGEMEIARETNP	360
Qy	360	VIGYDRNEKNTNAALKAAGITVLPFHGNQLSLGMGNARCMSP	409
Db	361	VIGYDRNEKNTNAALKAAGITVLPFHGNQLSLGMGNARCMSP	410

RESULT 9  
 US-09-271-713-8  
 ; Sequence 8, Application US/09271713  
 ; Patent No. 6132713  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Filpula, David  
 ; APPLICANT: Wang, Maoliang  
 ; TITLE OF INVENTION: Arginine Deiminase Derived From  
 ; TITLE OF INVENTION: Mycoplasma and Polymer Conjugates Containing the Same  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ROBERTS & MERCANTI  
 ; STREET: 81 Tamarack Circle  
 ; CITY: Skillman  
 ; STATE: New Jersey  
 ; COUNTRY: United States  
 ; ZIP: 08558  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/271,713  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/792,283  
 ; FILING DATE: 31-JAN-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mercanti, Michael N.  
 ; REGISTRATION NUMBER: 33966  
 ; REFERENCE/DOCKET NUMBER: 2131055  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 609-921-3500  
 ; TELEFAX: 609-921-9535  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 410 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: No. 6132713 Relevant  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Mycoplasma hominis  
 ; STRAIN: PG21  
 ; CELL TYPE: unicellular  
 US-09-271-713-8

		Query Match	99.0%; Score 2098.5; DB 3; Length 410;	
		Best Local Similarity	99.3%; Pred. No. 3.3e-210;	
		Matches 407; Conservative	0; Mismatches 2; Indels 1; Gaps 1;	
Qy	1	MSVFDSKFNHVVSEIGELTVLVVHEPGREIDYITPARDELIFSAILESHDKARHQHS	60	
Db	1	MSVFDSKFNHVVSEIGELTVLVVHEPGREIDYITPARDELIFSAILESHDKARHQE	60	
Qy	61	FVKIMKDGRINNVBLTDLVAETYDLASKAAKEFIETFTLPVLTEANKKAVRAFLLS	120	
Db	61	FVKIMKDGRINNVBLTDLVAETYDLASKAAKEFIETFTLPVLTEANKKAVRAFLLS	120	
Qy	121	KPTHEMVVERMMSGITYKELGVSENELIVDPMNLYTPTRDPFASVGNGVTTHFMRYIVR	179	

121	QKPTHEWVFPMMSGITKVELGVSENELIVDMPNVLFTTRDPPFASVGVNGVTIHFWRVIYVR	180
Db		
180	RRETLPARFVRNRHPKLVKTPWYDYPAMKMPIEGGDVFIYNNETLAVGVSRDLDITL	239
Qy		
181	RRETLPARFVRNRHPKLVKTPWYDYPAMKMPIEGGDVFIYNNETLAVGVSRDLDITL	240
Db		
240	LAKNIKANKEVEFKRIIVAINVPKWTNLMHLDITLMTLMDKNKFLYSPIANDVPKFDYDILV	299
Qy		
241	LAKNIKANKEVEFKRIIVAINVPKWTNLMHLDITLMTLMDKNKFLYSPIANDVPKFDYDILV	300
Db		
300	NGGAEPQPLNGLPLDKLLASIIINKEPVLPIPGAGATEMEIARETNFDGNTNYLAIKPOL	359
Qy		
301	NGGAEPQPLNGLPLDKLLASIIINKEPVLPIPGAGATEMEIARETNFDGNTNYLAIKPOL	360
Db		
360	VIGYDRNEKNTNAALKAAGITVLPHGNQLSLGGMNARCWSMPLSRKDVVKW	409
Qy		
361	VIGYDRNEKNTNAALKAAGITVLPHGNQLSLGGMNARCWSMPLSRKDVVKW	410
Db		

```

RESULT 10
US-09-023-809B-2
; Sequence 2, Application US/09023809B
; Patent No. 6183738
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A
; TITLE OF INVENTION: Modified Arginine Deiminase
; FILE REFERENCE: PHE00028
; CURRENT APPLICATION NUMBER: US/09/023,809B
; CURRENT FILING DATE: 2000-02-13
; PRIOR APPLICATION NUMBER: 60/046,200
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Mycoplasma arthritis
US-09-023-809B-2

```

Query Match	85.3%;	Score	1807.5;	DB	3;	Length	410;
Best Local Similarity	84.4%;	Pred. No.	8.1e-180;				
Matches	346;	Conservative	29;	Mismatches	34;	Indels	1;
Gaps	1;						
Qy	1	MSVFDKFNFGIHVYSEIGELT	VLVHEPGREIDYIT	PARDEL	LF	SAIL	ESH
Db	1	MSVFDKFKGIHVYSEIGEL	SVLVVHEPGREIDYIT	PARDEL	LF	SAIL	ESH
Qy	61	FWKIMKDRGINVVELTDL	VLAETDY	L	S	A	K
Db	61	FVAILKANDINVVELTDL	VLAETDY	L	S	A	K
Qy	121	KPT-HEMVFMGGITKYL	GVSENELIVD	PMNLY	FT	RD	P
Db	121	KKT	SRKLVELMAGITKY	DLGVSE	NELIVD	PMNLY	FT
Qy	180	RRET	LFAFVFRNHPKLV	KTPWY	DP	AMKMP	IEG
Db	181	RRET	LFSRFRNHPKLV	NTPTWY	DP	AMKLS	IEG
Qy	240	LAKNI	KANKEVEPKRIV	AINV	PK	WTNLM	HLDT
Db	241	LAKNL	VANKECEPKRIV	AINV	PK	WTNLM	HLDT
Qy	300	NGAE	POPQNLGLPK	LLAS	I	INKE	P
Db	301	NGAE	POPQVNGLE	PKL	Q	LS	I
Qy	360	VIGY	DRNEK	TNAAL	KA	AGI	V
Db	361	VIGY	SRNEK	TNAAL	KA	AGI	V

```
US-09-723-546-2
; Sequence 2, Application US/09723546
; Patent No. 6737259
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A
; TITLE OF INVENTION: Modified Arginine Deiminase
; FILE REFERENCE: PH080059
; CURRENT APPLICATION NUMBER: US/09/723,546
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/023,809
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-09-723-546-2
Query Match      85.3%; Score 1807.5; DB 4; Length 410;
Best Local Similarity 84.4%; Pred. No. 8.1e-180;
Matches 346; Conservative 29; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MSVPDSKFNHGVSEIGELTVLVHPEGREIDYITPARLDELLFSAILESHDARKEHQS 60
Db 1 MSVPDSKFNHGVSEIGELTVLVHPEGREIDYITPARLDELLFSAILESHDARKEHQS 60
Qy 61 FVKIMKDRGINNVVELTDLVAETIDYDLSAAKKEEFIEFTLEETVPVLTANKKAVRAFLLS 120
Db 61 FVAILKANDINNVETIDLVVAETIDYDLSAAKKEEFIEFTLEETVPVLTANKKAVRAFLLS 120
Qy 121 KPT-HEMVFFMMSGITKYELGVSENELIVDPMPNLVTRDPPFASVGVNGVTIHFMRVYVR 179
Db 121 KKTSRKLVLMAGITKYDLGVEADHLLVDPMPNLVTRDPPFASVGVNGVTIHFMRVYVR 180
Qy 180 RRETLFARFVRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 RRETLFARFVRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITL 240
Qy 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSPIANDVFKFWDYDLV 299
Db 241 LAKNLVANKECEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSPIANDVFKFWDYDLV 300
Qy 300 NGABEPQPNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNPDGTNYLAIKPGL 359
Db 301 NGABEPQPNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNPDGTNYLAIRPGV 360
Qy 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408
Db 361 VIGYSRNEKTNAAKAAAGIKVLFPFHGNQLSLGMGNARCMSPLSRKDVK 409

RESULT 13
US-09-564-559B-9
; Sequence 9, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PH080033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: PCT/US01/14116
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-09-564-559B-9
Query Match      84.4%; Score 1789.5; DB 4; Length 409;
Best Local Similarity 84.1%; Pred. No. 6.1e-178;
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MSVPDSKFNHGVSEIGELTVLVHPEGREIDYITPARLDELLFSAILESHDARKEHQS 60
Db 1 MSVPDSKFNHGVSEIGELTVLVHPEGREIDYITPARLDELLFSAILESHDARKEHQS 60
Qy 61 FVKIMKDRGINNVVELTDLVAETIDYDLSAAKKEEFIEFTLEETVPVLTANKKAVRAFLLS 120
Db 61 FVAILKANDINNVETIDLVVAETIDYDLSAAKKEEFIEFTLEETVPVLTANKKAVRAFLLS 120
Qy 121 KPT-HEMVFFMMSGITKYELGVSENELIVDPMPNLVTRDPPFASVGVNGVTIHFMRVYVR 179
Db 121 KKTSRKLVLMAGITKYDLGVEADHLLVDPMPNLVTRDPPFASVGVNGVTIHFMRVYVR 180
Qy 180 RRETLFARFVRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 RRETLFARFVRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITL 240
Qy 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSPIANDVFKFWDYDLV 299
Db 241 LAKNLVANKECEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSPIANDVFKFWDYDLV 300
Qy 300 NGABEPQPNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNPDGTNYLAIKPGL 359
Db 301 NGABEPQPNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNPDGTNYLAIRPGV 360
Qy 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408
Db 361 VIGYSRNEKTNAAKAAAGIKVLFPFHGNQLSLGMGNARCMSPLSRKDVK 409

US-09-564-559B-7
; Sequence 7, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PH080033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: PCT/US01/14116
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 409
; TYPE: PRT
```



THIS PAGE BLANK (uspto)



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2004, 15:34:09 ; Search time 157 Seconds  
(without alignments)  
934.524 Million cell updates/sec

Title: US-10-674-666-1  
Perfect score: 2120  
Sequence: 1 MSVFSKFNHIVHSEIGEL.....LGMGNARCMPLSRKDVKN 409

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04: \*  
1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2120	100.0	409	5	AAE16134	AAE16134 Mycoplasma
2	2120	100.0	409	5	ABG31996	ABG31996 M. hominu
3	2112	99.6	409	5	AAE16136	AAE16136 Mycoplasma
4	2110	99.5	409	5	AAE16135	AAE16135 Mycoplasma
5	2109	99.5	408	2	AAW89442	AAW89442 Mycoplasma
6	2108	99.4	409	5	AAE16137	AAE16137 Mycoplasma
7	1807.5	85.3	410	5	ABG31995	ABG31995 M. arthri
8	1796.5	84.7	409	2	AAW89441	AAW89441 Mycoplasma
9	1764.5	83.2	410	5	ABG31994	ABG31994 M. argini
10	1763.5	83.2	410	5	ABW76127	ABW76127 Mycoplasma
11	1753.5	82.7	409	2	AAW89440	AAW89440 Mycoplasma
12	1733.5	81.8	409	2	AAW24528	AAW24528 Arginine
13	1732.5	81.7	410	2	AAW65454	AAW65454 Arginine
14	1632.5	77.0	405	2	AAW05713	AAW05713 Arginine
15	1081.5	51.0	264	2	AAW20500	AAW20500 Cell grow
16	1067.5	50.4	263	2	AAW10854	AAW10854 Arginine
17	682.5	32.2	432	8	ADM77935	ADM77935 S. suis A
18	681.5	32.1	413	5	ABG32003	ABG32003 B. lichen
19	679	32.0	411	1	AAW70278	AAW70278 Streptoco
20	679	32.0	411	5	ABP26975	ABP26975 Streptoco
21	679	32.0	411	5	ABG31997	ABG31997 S. pyogen
22	679	32.0	411	7	ADC56694	ADC56694 Streptoco
23	678.5	32.0	410	5	ABP26974	ABP26974 Streptoco
24	670.5	31.6	408	5	ABG32004	ABG32004 E. faecal
25	667.5	31.5	417	7	ADC96521	ADC96521 E. faeciu

26	655	30.9	413	5	ABG32002	ABG32002 C. perfri
27	652.5	30.8	409	8	ADK47759	ADK47759 Streptoco
28	651.5	30.7	409	5	ABG31998	ABG31998 S. pneumo
29	651.5	30.7	409	6	ABU02672	ABU02672 S. pneumo
30	644.5	30.4	411	6	ABW72707	ABW72707 Staphyloc
31	640.5	30.2	411	2	AAW99068	AAW99068 Staphyloc
32	640.5	30.2	422	5	ABP38086	ABP38086 Staphyloc
33	640	30.2	408	6	ADB10770	ADB10770 Alloioococ
34	640	30.2	417	5	ADB10768	ADB10768 Alloioococ
35	632	29.8	410	5	ABB49849	ABB49849 Listeria
36	631.5	29.8	410	5	ABB55391	ABB55391 Lactococ
37	625	29.5	409	5	ABG32005	ABG32005 L. sake a
38	618	29.2	420	5	ABP39582	ABP39582 Staphyloc
39	612.5	28.9	410	5	ABG31999	ABG31999 B. burgdo
40	604.5	28.5	394	4	AAW81482	AAW81482 S. epider
41	600.5	28.3	409	5	ABG32000	ABG32000 B. afzeli
42	581.5	27.4	379	7	ADH88142	ADH88142 Enterococ
43	519	24.5	406	4	ABB52662	ABB52662 Escherich
44	476.5	22.5	415	4	AAU58873	AAU58873 Propionib
45	476.5	22.5	415	6	ABM55392	ABM55392 Propionib

ALIGNMENTS

RESULT 1  
AAE16134  
ID AAE16134 standard; protein; 409 AA.

XX AC AAE16134;

XX DT 26-MAR-2002 (first entry)

XX DE Mycoplasma hominis wild type arginine deiminase (ADI).

XX KW Arginine deiminase; ADI; cytostatic; antibacterial; immunosuppressive;  
XX KW antiparasitic; cancer; melanoma; hepatoma; sarcoma; parasitic disease;  
XX KW septic shock; tumour.

XX OS Mycoplasma hominis.

XX PN WO200183774-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US014116.

XX PR 04-MAY-2000; 2000US-00564559.

XX PA (PHOB-) PHOENIX PHARMACOLOGICS INC.

XX PI Ensor CM, Holtsberg FW, Clark MA;

XX DR WPI; 2002-097497/13.

XX PT Modified arginine deiminase for improved manufacturing processes and for  
XX PT treating cancer, is mutated to be free of a pegylation site at or  
XX PT adjacent to its catalytic region.

XX PS Example 3; Fig 1; 34pp; English.

XX CC The invention relates to a modified arginine deiminase (ADI) for improved  
XX CC manufacturing processes. The process comprises ADI modified to be free of  
XX CC at least one pegylation site at or adjacent to its catalytic region. ADI  
XX CC catalyses the conversion of arginine to citrulline and may be used to  
XX CC eliminate arginine. ADI is useful for treating cancer, melanomas,  
XX CC hepatomas, sarcomas, parasitic diseases, septic shock and for treating  
XX CC and inhibiting metastasis of tumour cells and other disease states. The  
XX CC present sequence is Mycoplasma hominis wild type ADI

XX SQ Sequence 409 AA;

Query Match 100.0%; Score 2120; DB 5; Length 409;

Best Local Similarity 100.0%; Pred. No. 1.4e-193; Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MSVPDSKFNHIVYSEIGELETVLVHPGREGIDYITPARDELFSAILSHDARKEHQ 60
Db	1 MSVPDSKFNHIVYSEIGELETVLVHPGREGIDYITPARDELFSAILSHDARKEHQ 60
Qy	61 FVKIMKDRGINVVELTDLVAETVDLASKAAKEFIETFLPETVPLTEANKKAVRAFLS 120
Db	61 FVKIMKDRGINVVELTDLVAETVDLASKAAKEFIETFLPETVPLTEANKKAVRAFLS 120
Qy	121 KPHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPFASVGVNGVTIHFMRIVRR 180
Db	121 KPHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPFASVGVNGVTIHFMRIVRR 180
Qy	181 RETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVSERTDITILL 240
Db	181 RETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVSERTDITILL 240
Qy	241 AKNIKANKEVEFKRIIVAINVPKWNLMLHDLTWTMLDKNKFLYSPIANDVFKWDYDLVN 300
Db	241 AKNIKANKEVEFKRIIVAINVPKWNLMLHDLTWTMLDKNKFLYSPIANDVFKWDYDLVN 300
Qy	301 GGAEPOPQLNGLPLDKLLASIINKEPVLPIGGAGATEMEIARETNFDGNTYLAIKPGLV 360
Qy	361 IGYDRNEKNTAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409
Db	361 IGYDRNEKNTAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409
RESULT 2	
ABG31996	
ID	ABG31996 standard; protein; 409 AA.
XX	AC ABG31996;
XX	DT 06-AUG-2003 (revised)
DT	15-NOV-2002 (first entry)
XX	XX
DE	M. hominus arginine deiminase gene, HOWADIPRO.
XX	Arginine deiminase; cytosolic; ADI; polyethylene glycol; PEG; arginine;
KW	citrulline; argininosuccinate synthase; argininosuccinate lyase; cancer;
KW	autotrophic; tumour; melanoma; hepatoma; sarcoma; metastasis; antigenic.
XX	XX
OS	Mycoplasma hominis.
XX	XX
XX	WO200244360-A2.
XX	PD 06-JUN-2002.
XX	XX
PF	19-SEP-2001; 2001WO-US029184.
XX	XX
PR	28-NOV-2000; 2000US-00723546.
XX	XX
PA	(PHOE-) PHOENIX PHARMACOLOGICS INC.
XX	XX
PI	Clark MA;
XX	XX
DR	WPI; 2002-619003/66.
XX	XX
PT	Compound for treating tumor such as melanoma, hepatoma or sarcoma in a
PT	patient, comprises arginine deiminase covalently bonded by a linking
PT	group such as succinimide to polyethylene glycol.
XX	XX
PS	Example 1; Fig 1; 59pp; English.
XX	XX
CC	The invention discloses a compound comprising arginine deiminase (ADI)
CC	covalently bonded by a linking group to polyethylene glycol (PEG) having
CC	a total weight average molecular weight of about 1000-50000. Also
CC	disclosed is a method for enhancing the circulating half life or the

CC	tumoricidal activity of arginine deiminase by modifying the arginine
CC	deiminase by covalently bonding the arginine deiminase by a linking group
CC	to PEG. Normal cells can synthesize arginine from citrulline in a 2 step
CC	process catalysed by argininosuccinate synthase and argininosuccinate
CC	lyase. In contrast, many cancerous cells do not express argininosuccinate
CC	synthase and are, therefore, auxotrophic for arginine. Arginine deiminase
CC	catalyses the conversion of arginine to citrulline and can be used to
CC	eliminate arginine from the cancerous cells. The compound is useful for
CC	treating a tumour such as melanoma, hepatoma or sarcoma in a patient, or
CC	for treating and inhibiting metastases in a patient. When compared to
CC	native arginine deiminase the compound retains most of its enzymatic
CC	activity, is far less antigenic, has a greatly extended circulating half-
CC	life, and is much more efficacious in the treatment of tumours. The
CC	sequence presented is the Mycoplasma hominus arginine deiminase gene,
CC	HOWADIPRO. (Updated on 06-AUG-2003 to correct OS field.)
XX	XX
SQ	Sequence 409 AA;
Query Match 100.0%; Score 2120; DB 5; Length 409;	
Best Local Similarity 100.0%; Pred. No. 1.4e-193;	
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MSVPDSKFNHIVYSEIGELETVLVHPGREGIDYITPARDELFSAILSHDARKEHQ 60
Db	1 MSVPDSKFNHIVYSEIGELETVLVHPGREGIDYITPARDELFSAILSHDARKEHQ 60
Qy	61 FVKIMKDRGINVVELTDLVAETVDLASKAAKEFIETFLPETVPLTEANKKAVRAFLS 120
Db	61 FVKIMKDRGINVVELTDLVAETVDLASKAAKEFIETFLPETVPLTEANKKAVRAFLS 120
Qy	121 KPHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPFASVGVNGVTIHFMRIVRR 180
Db	121 KPHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPFASVGVNGVTIHFMRIVRR 180
Qy	181 RETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVSERTDITILL 240
Db	181 RETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVSERTDITILL 240
Qy	241 AKNIKANKEVEFKRIIVAINVPKWNLMLHDLTWTMLDKNKFLYSPIANDVFKWDYDLVN 300
Db	241 AKNIKANKEVEFKRIIVAINVPKWNLMLHDLTWTMLDKNKFLYSPIANDVFKWDYDLVN 300
Qy	301 GGAEPOPQLNGLPLDKLLASIINKEPVLPIGGAGATEMEIARETNFDGNTYLAIKPGLV 360
Qy	361 IGYDRNEKNTAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409
Db	361 IGYDRNEKNTAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409
RESULT 3	
AAE16136	
ID	AAE16136 standard; protein; 409 AA.
XX	AC AAE16136;
XX	DT 26-MAR-2002 (first entry)
XX	XX
DE	Mycoplasma hominis modified arginine deiminase (ADI) #2.
XX	XX
KW	Arginine deiminase; ADI; cytosolic; antibacterial; immunosuppressive;
KW	antiparasitic; cancer; melanoma; hepatoma; sarcoma; parasitic disease;
KW	septic shock; tumour; mutant; mutein.
XX	XX
OS	Mycoplasma hominis.
OS	Synthetic.
XX	XX
PH	Key Location/Qualifiers
FT	Misc-difference 210
FT	/note= "wild type Pro substituted with Ser"
XX	XX
PN	WO200183774-A2.

XX 08-NOV-2001.  
XX  
XX  
XX  
XX 02-MAY-2001; 2001WO-US014116.  
XX  
XX  
XX 04-MAY-2000; 2000US-00564559.  
XX  
XX  
XX (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX PA  
XX Ensor CM, Holsberg FW, Clark MA;  
XX  
XX WPI; 2002-097497/13.  
XX  
XX Modified arginine deiminase for improved manufacturing processes and for  
PT treating cancer, is mutated to be free of a pegylation site at or  
PT adjacent to its catalytic region.  
XX  
XX Disclosure; Page 31-32; 34pp; English.  
XX  
XX The invention relates to a modified arginine deiminase (ADI) for improved  
CC manufacturing processes. The process comprises ADI modified to be free of  
CC at least one pegylation site at or adjacent to its catalytic region. ADI  
CC catalyses the conversion of arginine to citrulline and may be used to  
CC eliminate arginine. ADI is useful for treating cancer, melanomas,  
CC hepatomas, sarcomas, parasitic diseases, septic shock and for treating  
CC and inhibiting metastasis of tumour cells and other disease states. The  
CC present sequence is Mycoplasma hominis modified ADI protein  
XX  
XX Sequence 409 AA;  
XX  
Query Match 99.6%; Score 2112; DB 5; Length 409;  
Best Local Similarity 99.8%; Pred. No. 8.1e-193;  
Matches 408; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MSVFDKFGNGIHVYSGISETLVLVHEPGREIDYITPARLDELLFSAILES HDARKEHQS 60  
Db 1 MSVFDKFGNGIHVYSGISETLVLVHEPGREIDYITPARLDELLFSAILES HDARKEHQS 60  
QY 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETFEETVPVLTEANKKAVRAFLS 120  
Db 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETFEETVPVLTEANKKAVRAFLS 120  
QY 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMPNLYFTRDPFASVGVNGVTIHPMRYIVRR 180  
Db 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMPNLYFTRDPFASVGVNGVTIHPMRYIVRR 180  
QY 181 RETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLDITILL 240  
Db 181 RETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLDITILL 240  
QY 241 AKNIKANKEVEFKRIVAINVVKWNLMLHDLTWTMLDKNKFYSPIANDVFKFWDYDLVN 300  
Db 241 AKNIKANKEVEFKRIVAINVVKWNLMLHDLTWTMLDKNKFYSPIANDVFKFWDYDLVN 300  
QY 301 GGAEPQQLNGPLDKLLASIIKKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
Db 301 GGAEPQQLNGPLDKLLASIIKKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
QY 361 IGYDRNEKNTAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 409  
Db 361 IGYDRNEKNTAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 409  
RESULT 4  
AAE16135  
ID AAE16135 standard; protein; 409 AA.  
XX  
XX  
XX AAE16135;  
XX  
XX  
XX 26-MAR-2002 (first entry)  
XX  
XX Mycoplasma hominis modified arginine deiminase (ADI) #1.  
XX

KW Arginine deiminase; ADI; cytostatic; antibacterial; immunosuppressive;  
KW antiparasitic; cancer; melanoma; hepatoma; sarcoma; parasitic disease;  
KW septic shock; tumour; mutant; mutein.  
XX  
XX  
XX Mycoplasma hominis.  
OS Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 111  
FT Misc-difference /note= "Wild type Lys substituted with Pro"  
FT Misc-difference 112 /note= "Wild type Lys substituted with Glu"  
FT  
XX  
XX WO200183774-A2.  
XX  
XX 08-NOV-2001.  
XX  
XX 02-MAY-2001; 2001WO-US014116.  
XX  
XX 04-MAY-2000; 2000US-00564559.  
XX (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX  
XX Ensor CM, Holsberg FW, Clark MA;  
XX WPI; 2002-097497/13.  
XX  
XX Modified arginine deiminase for improved manufacturing processes and for  
PT treating cancer, is mutated to be free of a pegylation site at or  
PT adjacent to its catalytic region.  
XX  
XX Disclosure; Page 30-31; 34pp; English.  
XX  
XX The invention relates to a modified arginine deiminase (ADI) for improved  
CC manufacturing processes. The process comprises ADI modified to be free of  
CC at least one pegylation site at or adjacent to its catalytic region. ADI  
CC catalyses the conversion of arginine to citrulline and may be used to  
CC eliminate arginine. ADI is useful for treating cancer, melanomas,  
CC hepatomas, sarcomas, parasitic diseases, septic shock and for treating  
CC and inhibiting metastasis of tumour cells and other disease states. The  
CC present sequence is Mycoplasma hominis modified ADI protein  
XX  
XX Sequence 409 AA;  
XX  
Query Match 99.5%; Score 2110; DB 5; Length 409;  
Best Local Similarity 99.5%; Pred. No. 1.3e-192;  
Matches 407; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MSVFDKFGNGIHVYSGISETLVLVHEPGREIDYITPARLDELLFSAILES HDARKEHQS 60  
Db 1 MSVFDKFGNGIHVYSGISETLVLVHEPGREIDYITPARLDELLFSAILES HDARKEHQS 60  
QY 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETFEETVPVLTEANKKAVRAFLS 120  
Db 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETFEETVPVLTEANKKAVRAFLS 120  
QY 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMPNLYFTRDPFASVGVNGVTIHPMRYIVRR 180  
Db 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMPNLYFTRDPFASVGVNGVTIHPMRYIVRR 180  
QY 181 RETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLDITILL 240  
Db 181 RETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLDITILL 240  
QY 241 AKNIKANKEVEFKRIVAINVVKWNLMLHDLTWTMLDKNKFYSPIANDVFKFWDYDLVN 300  
Db 241 AKNIKANKEVEFKRIVAINVVKWNLMLHDLTWTMLDKNKFYSPIANDVFKFWDYDLVN 300  
QY 301 GGAEPQQLNGPLDKLLASIIKKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
Db 301 GGAEPQQLNGPLDKLLASIIKKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
QY 361 IGYDRNEKNTAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 409

```

|||||
361 IGYDRNEKTNALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 409
|||||

Db
RESULT 5
AAW89442
ID AAW89442 standard; protein; 408 AA.
AC AAW89442;
XX
XX
DT 18-MAR-1999 (first entry)
XX
DE Mycoplasma hominis arginine deiminase.
XX
XX Arginine deiminase; Mycoplasma arginini; Mycoplasma arthritis;
KW Mycoplasma hominis; modified; polyethylene glycol; cancer; metastasis;
KW inhibition; melanoma; hepatoma; sarcoma; enhanced circulating half life.
XX
XX Mycoplasma hominis.
OS
XX
XX WO9851784-A1.
XX
XX 19-NOV-1998.
XX
XX 12-MAY-1998; 98WO-US009575.
XX
XX 12-MAY-1997; 97US-0046200P.
PR 13-FEB-1998; 98US-00023809.
XX
XX (PHOB-) PHOENIX PHARMACOLOGICS INC.
XX
XX Clark MA;
XX
XX WPI; 1999-045227/04.
XX
XX New compound comprising arginine deiminase - covalently bonded via
PT linking group to polyethylene glycol, to enhance the half life of
PT arginine by this modification.
XX
XX Claim 6; Fig 1; 30pp; English.
XX
XX The present sequence represents Mycoplasma hominis arginine deiminase.
CC The present invention describes: (1) a compound comprising arginine
CC deiminase (AD) covalently bonded via linking group to polyethylene glycol
CC (PEG), and having a molecular weight 12-40 kDa; and (2) a composition as
CC above, but where the linking group is selected from a malimide group, an
CC amide group, an imide group, a carbamate group, an ester group, an epoxy
CC group, a carboxyl group, a hydroxyl group, a carboxylate, a tyrosine
CC group, a cysteine group and/or a histidine group. AD can be used in the
CC treatment of tumours, e.g. melanomas, hepatomas and sarcomas, and to
CC inhibit metastasis. The modified AD has an enhanced circulating half life
XX
XX Sequence 408 AA;
XX
XX Query Match 99.5%; Score 2109; DB 2; Length 408;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-192; Mismatches 0; Indels 0; Gaps 0;
XX Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSVDSKFNHGVSEIGELETVLVHPEGRIDYITPARLDELFSAILSHDARKHQHS 60
Db 1 MSVDSKFNHGVSEIGELETVLVHPEGRIDYITPARLDELFSAILSHDARKHQHS 60
Qy 61 FVKIMKRGINVELTDLVAETDYLASKAAKEETETLEETVPLTEANKKAVRAFLLS 120
Db 61 FVKIMKRGINVELTDLVAETDYLASKAAKEETETLEETVPLTEANKKAVRAFLLS 120
Qy 121 KPTHEWVFMSGITYKELGVSENELIVDPMNLYFTRDPFASVGVNGVTIHFMYIVRR 180
Db 121 KPTHEWVFMSGITYKELGVSENELIVDPMNLYFTRDPFASVGVNGVTIHFMYIVRR 180
Qy 181 RETLFAFVFRNHPKLVKTPWYDPAKQPIEGGDVFIYNNETLVVGVSERTDLDITLL 240
Db 181 RETLFAFVFRNHPKLVKTPWYDPAKQPIEGGDVFIYNNETLVVGVSERTDLDITLL 240

Qy 241 AKNIKANKEVEPKRIVAINVPKWTNLMHLDTWLTKNKFLYSPIANDVFKFWDYDLVN 300
Db 241 AKNIKANKEVEPKRIVAINVPKWTNLMHLDTWLTKNKFLYSPIANDVFKFWDYDLVN 300
Qy 301 GGAEFPQQLNGLPDLKLASIIKEPVLPIPIGGAGATEMEIARETNFGDTNYLAIKPGLV 360
Db 301 GGAEFPQQLNGLPDLKLASIIKEPVLPIPIGGAGATEMEIARETNFGDTNYLAIKPGLV 360
Qy 361 IGYDRNEKTNALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408
Db 361 IGYDRNEKTNALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408

RESULT 6
AAE16137
ID AAE16137 standard; protein; 409 AA.
XX
XX AAE16137;
XX
XX 26-MAR-2002 (first entry)
DT
XX
DE Mycoplasma hominis modified arginine deiminase (ADI) E112, S210.
XX
XX Arginine deiminase; ADI; cytostatic; antibacterial; immunosuppressive;
KW antiparasitic; cancer; melanoma; hepatoma; sarcoma; parasitic disease;
KW septic shock; tumour; mutant; mutein.
XX
XX Mycoplasma hominis.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 112
FT Misc-difference /notes= "Wild type Lys substituted with Glu"
FT Misc-difference 210 /notes= "Wild type Pro substituted with Ser"
XX
XX WO200183774-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US014116.
XX
XX 04-MAY-2000; 2000US-00564559.
XX
XX (PHOB-) PHOENIX PHARMACOLOGICS INC.
XX
XX Ensor CM, Holteberg FW, Clark MA;
XX WPI; 2002-097497/13.
XX
XX Modified arginine deiminase for improved manufacturing processes and for
PT treating cancer, is mutated to be free of a pegylation site at or
PT adjacent to its catalytic region.
XX
XX Example 1; Fig 2; 34pp; English.
XX
XX The invention relates to a modified arginine deiminase (ADI) for improved
CC manufacturing processes. The process comprises ADI modified to be free of
CC at least one pegylation site at or adjacent to its catalytic region. ADI
CC catalyses the conversion of arginine to citrulline and may be used to
CC eliminate arginine. ADI is useful for treating cancer, melanomas,
CC hepatomas, sarcomas, parasitic diseases, septic shock and for treating
CC and inhibiting metastasis of tumour cells and other disease states. The
CC present sequence is Mycoplasma hominis modified ADI protein
XX
XX Sequence 409 AA;
XX
XX Query Match 99.4%; Score 2108; DB 5; Length 409;
XX Best Local Similarity 99.5%; Pred. No. 1.9e-192;
XX Matches 407; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSVDSKFNHGVSEIGELETVLVHPEGRIDYITPARLDELFSAILSHDARKHQHS 60

```

Db 1 MSVFDKFGNIHYSEIGLETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60  
Qy 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETLEETVPLTEANKKAVRAFLS 120  
Db 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETLEETVPLTEANKKAVRAFLS 120  
Qy 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPPFASVGVNGVTIHFMRVIVR 180  
Db 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPPFASVGVNGVTIHFMRVIVR 180  
Qy 181 RETLFAFVRNHPKLVKTPWYDPAKMPKEGGDVFIYNNETLVVGVSERTDLDITILL 240  
Db 181 RETLFAFVRNHPKLVKTPWYDPAKMPKEGGDVFIYNNETLVVGVSERTDLDITILL 240  
Qy 241 AKNIKANKVEFKRIVAINVPKWTNLMHLDTWLMDKNKLYSPANDVFKFWDYDLVN 300  
Db 241 AKNIKANKVEFKRIVAINVPKWTNLMHLDTWLMDKNKLYSPANDVFKFWDYDLVN 300  
Qy 301 GGAEPOPQNLGLPLDKLASIINKEPVLPIPGGAGATEMEIARETNFDGNTNYLAIKPGLV 360  
Db 301 GGAEPOPQNLGLPLDKLASIINKEPVLPIPGGAGATEMEIARETNFDGNTNYLAIKPGLV 360  
Qy 361 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 409  
Db 361 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 409

RESULT 7  
ABG31995  
ID ABG31995 standard; protein; 410 AA.  
XX  
AC ABG31995;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE M. arthritides arginine deiminase gene, ARTADIPRO.  
XX  
KW Arginine deiminase; cytosolic; ADI; polyethylene glycol; PEG; arginine;  
KW citrulline; argininosuccinate synthase; argininosuccinate lyase; cancer;  
KW autotrophic; tumour; melanoma; hepatoma; sarcoma; metastasis; antigenic.  
XX  
OS Mycoplasma arthritidis.  
XX  
PN WO200244360-A2.  
PD  
PF 06-JUN-2002.  
PF 19-SEP-2001; 2001WO-US029184.  
PR 28-NOV-2000; 2000US-00723546.  
XX  
PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX  
PI Clark MA;  
XX  
WPI; 2002-619003/66.  
XX  
PT Compound for treating tumor such as melanoma, hepatoma or sarcoma in a  
PT patient, comprises arginine deiminase covalently bonded by a linking  
PT group such as succinimide to polyethylene glycol.  
XX  
PS Example 1; Fig 1; 59pp; English.  
XX  
CC The invention discloses a compound comprising arginine deiminase (ADI)  
CC covalently bonded by a linking group to polyethylene glycol (PEG) having  
CC a total weight average molecular weight of about 1000-50000. Also  
CC disclosed is a method for enhancing the circulating half life or the  
CC tumoricidal activity of arginine deiminase by modifying the arginine  
CC deiminase by covalently bonding the arginine deiminase by a linking group  
CC to PEG. Normal cells can synthesise arginine from citrulline in a 2 step  
CC process catalysed by argininosuccinate synthase and argininosuccinate  
CC lyase. In contrast, many cancerous cells do not express argininosuccinate

CC synthase and are, therefore, autotrophic for arginine. Arginine deiminase  
CC catalyses the conversion of arginine to citrulline and can be used to  
CC eliminate arginine from the cancerous cells. The compound is useful for  
CC treating a tumour such as melanoma, hepatoma or sarcoma in a patient, or  
CC for treating and inhibiting metastases in a patient. When compared to  
CC native arginine deiminase the compound retains most of its enzymatic  
CC activity, is far less antigenic, has a greatly extended circulating half-  
CC life, and is much more efficacious in the treatment of tumours. The  
CC sequence presented is the Mycoplasma arthritidis arginine deiminase gene,  
CC ARTADIPRO  
XX  
SQ Sequence 410 AA;  
Query Match 85.3%; Score 1807.5; DB 5; Length 410;  
Best Local Similarity 84.4%; Pred. No. 11e-163;  
Matches 346; Conservative 29; Mismatches 34; Indels 1; Gaps 1;  
Qy 1 MSVFDKFGNIHYSEIGLETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60  
Db 1 MSVFDKFGNIHYSEIGLETVLVHEPGREIDYITPARLDELLFSAILESHDARKEQSQ 60  
Qy 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETLEETVPLTEANKKAVRAFLS 120  
Db 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETLEETVPLTEANKKAVRAFLS 120  
Qy 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPPFASVGVNGVTIHFMRVIVR 179  
Db 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPPFASVGVNGVTIHFMRVIVR 179  
Qy 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPPFASVGVNGVTIHFMRVIVR 180  
Db 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPPFASVGVNGVTIHFMRVIVR 180  
Qy 181 RETLFAFVRNHPKLVKTPWYDPAKMPKEGGDVFIYNNETLVVGVSERTDLDITILL 239  
Db 181 RETLFAFVRNHPKLVKTPWYDPAKMPKEGGDVFIYNNETLVVGVSERTDLDITILL 240  
Qy 240 IAKNIKANKVEFKRIVAINVPKWTNLMHLDTWLMDKNKLYSPANDVFKFWDYDLV 299  
Db 240 IAKNIKANKVEFKRIVAINVPKWTNLMHLDTWLMDKNKLYSPANDVFKFWDYDLV 300  
Qy 300 NGAEPOPQNLGLPLDKLASIINKEPVLPIPGGAGATEMEIARETNFDGNTNYLAIKPGL 359  
Db 301 NGAEPOPQNLGLPLDKLASIINKEPVLPIPGGAGATEMEIARETNFDGNTNYLAIRPGV 360  
Qy 360 VGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 409  
Db 361 VGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 410  
RESULT 8  
AAW89441  
ID AAW89441 standard; protein; 409 AA.  
XX  
AC AAW89441;  
XX  
DT 18-MAR-1999 (first entry)  
XX  
DE Mycoplasma arthritidis arginine deiminase.  
XX  
KW Arginine deiminase; Mycoplasma arginini; Mycoplasma arthritidis;  
KW Mycoplasma hominis; modified; polyethylene glycol; cancer; metastasis;  
KW inhibition; melanoma; hepatoma; sarcoma; enhanced circulating half life.  
XX  
OS Mycoplasma arthritidis.  
XX  
PN WO9851784-A1.  
XX  
PD 19-NOV-1998.  
XX  
PF 12-MAY-1998; 98WO-US009575.  
XX  
PR 12-MAY-1997; 97US-0046200P.  
PR 13-FEB-1998; 98US-00023809.  
XX  
PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX

```

PI Clark MA;
XX WPI; 1999-045227/04.
XX
XX
XX New compound comprising arginine deiminase - covalently bonded via
PT linking group to polyethylene glycol, to enhance the half life of
PT arginine by this modification.
XX
XX Claim 6; Fig 1; 30pp; English.
XX
XX The present sequence represents Mycoplasma arthritis arginine
XX deiminase. The present invention describes: (1) a compound comprising
XX arginine deiminase (AD) covalently bonded via linking group to
XX polyethylene glycol (PEG), and having a molecular weight 12-40 kDa; and
XX (2) a composition as above, but where the linking group is selected from
XX a malimide group, an amide group, an imide group, a carbamate group, an
XX ester group, an epoxy group, a carboxyl group, a hydroxyl group, a
XX carbohydrate, a tyrosine group, a cysteine group and/or a histidine
XX group. AD can be used in the treatment of tumours, e.g. melanomas,
XX hepatomas and sarcomas, and to inhibit metastasis. The modified AD has an
XX enhanced circulating half life
XX
XX Sequence 409 AA;
XX
XX Query Match 84.7%; Score 1796.5; DB 2; Length 409;
XX Best Local Similarity 84.4%; Pred. No. 1.2e-162; Mismatches 34; Indels 1; Gaps 1;
XX Matches 345; Conservative 29;
XX
QY 1 MSVPDSKFGIHVYSEIGELETVLVHPGREGIDYITPARDELLEFSAILESHDARKEHQS 60
DB 1 MSVPDSKFGIHVYSEIGELESVLVHPGREGIDYITPARDELLEFSAILESHDARKEHQS 60
QY 61 FVKIMKDRGINVVELTDLVAETYLASAKAEEFIETLEETVPLTEANKKAVRAFLLS 120
DB 61 FVAILKANDINNVVELTDLVAETYLASAKAEEFIETLEETVPLTEANKKAVRAFLLS 120
QY 121 KPT-HEMVEPMMSGITKVELGVSENELIVDPMNLYFTDRPPASVGVNGVTIHFMYRIVR 179
DB 121 KTSRKLVEIMMAGITKYDLGVEADHELIVDPMNLYFTDRPPASVGVNGVTIHFMYRIVR 180
QY 180 RRETLFARFVRNHPKLVKTPWYDDPAMKMPIEGGDVFIYNNETLVVGVSERTDLDITL 239
DB 181 RRETLFSRFRNHPKLVNTPWYDDPAMKLSIEGGDVFIYNNETLVVGVSERTDLDITL 240
QY 240 LAKNIKANKEVEFKRIIVAINVVKWTNLMHLDITLMDKKNKFLYSPINDVFKFWDYDLV 299
DB 241 LAKNLVANKCECFKRIIVAINVVKWTNLMHLDITLMDKKNKFLYSPINDVFKFWDYDLV 300
QY 300 NGGAEPQPOLNGLPLDKLLASIIKKEPVLIPIGGAGATEMEIARETNPDGNTYLAIRPGV 359
DB 301 NGGAEPQPVENGLPLEKLLQSIINKKPVLIPIAGEGASQMEIERETHFDGNTYLAIRPGV 360
QY 360 VIGYDRNEKNTNAALKAAGITVLPFHGNQSLGNGNARCMSPLSRKDVK 408
DB 361 VIGYSRNEKNTNAALKAAGIKVLPFHGNQSLGNGNARCMSPLSRKDVK 409

RESULT 9
ABG31994
ID ABG31994 standard; protein; 410 AA.
AC ABG31994;
XX
XX 15-NOV-2002 (first entry)
XX
XX M. arginini arginine deiminase gene, ADIPROT.
XX
XX Arginine deiminase; cytotstatic; ADI; polyethylene glycol; PEG; arginine;
XX citrulline; argininosuccinate synthase; argininosuccinate lyase; cancer;
XX auxotrophic; tumour; melanoma; hepatoma; sarcoma; metastasis; antigenic.
XX
XX Mycoplasma arginini.
XX
```

QY	180	AAH76127 standard; protein; 410 AA.
Db	181	QRETLFSRFVSNHPKLIINPWYDPSLUKSLTEGGDFVIYNNDLTVGVSVSRDTDLQTIVTL
QY	240	LAKNIKANKEVEFKRIVAINVPKWNTLMHLDTWLTMLDKNKFXYSPANDVFKEWDYDLV
Db	241	LAKSIVANKECEFKRIVAINVPKWNTLMHLDTWLTMLDKNKFXYSPANDVFKEWDYDLV
QY	300	NGGASPOPOLINGPLDKLLASTIINKEPVLIPIGGAGATEMEIARETNPDGTNYLAIKPGL
Db	301	NGGASPPQPVENGPLEGLLSIINKKPVLIPPIAGEGASQMBIERETHFDGTNYLAIRPGV
QY	360	VIGYDRNEKTNAALKAAGITVLPFHGNQLSLGMGNARCMWSMPLSRKDVKW
Db	361	VIGYSRENKTNAALEAAGIKVLFPFHGNQLSLGMGNARCMWSMPLSRKDVKW
XX	RESULT 11	
XX	AAW89440	
ID	AAW89440	standard; protein; 409 AA.
XX	AAW89440;	
XX	18-MAR-1999	(first entry)
DT	DT	
XX	DE	Mycoplasma arginini arginine deiminase.
XX	KW	Arginine deiminase; Mycoplasma arginini; Mycoplasma arthritis;
KW	KW	Mycoplasma hominis; modified; polyethylene glycol; cancer; metastasis;
KW	KW	Inhibition; melanoma; hepatoma; sarcoma; enhanced circulating half life.
XX	OS	Mycoplasma arginini.
PN	PN	WO9851784-A1.
XX	XX	
PD	PD	19-NOV-1998.
XX	XX	
PF	PF	12-MAY-1998; 98WO-US0009575.
XX	XX	
PR	PR	12-MAY-1997; 97US-0046200P.
PR	PR	13-FEB-1998; 98US-00023809.
XX	XX	(PHOR-) PHOENIX PHARMACOLOGICS INC.
PA	PA	Clark MA;
XX	PI	WPI; 1999-045227/04.
XX	XX	New compound comprising arginine deiminase - covalently bonded via
PT	PT	linking group to polyethylene glycol, to enhance the half life of
PT	PT	arginine by this modification.
XX	XX	Claim 6; Fig 1; 30pp; English.
PS	PS	
XX	XX	The present sequence represents Mycoplasma arginini arginine deiminase.
CC	CC	The present invention describes: (1) a compound comprising arginine
CC	CC	deiminase (AD) covalently bonded via linking group to polyethylene glycol
CC	CC	(PEG), and having a molecular weight 12-40 kDa; and (2) a composition as
CC	CC	above, but where the linking group is selected from a malimide group, an
CC	CC	amide group, an imide group, a carbamate group, an ester group, an epoxy
CC	CC	group, a carboxyl group, a hydroxyl group, a carbohydrate, a tyrosine
CC	CC	group, a cysteine group and/or a histidine group. AD can be used in the
CC	CC	treatment of tumours, e.g. melanomas, hepatomas and sarcomas, and to
CC	CC	inhibit metastasis. The modified AD has an enhanced circulating half life
XX	XX	
SQ	SQ	Sequence 409 AA;
XX	XX	
Query Match	82.7%;	Score 1753.5; DB 2; Length 409;
Best Local Similarity	81.9%;	Pred. No. 1.5e-159;
Matches	335;	Conservative 37; Mismatches 36; Indels 1; Gaps 1;
QY	1	MSVDSKFNHGYHVSIGELETVLVHEPGREIDYITPARDELFFSAILESHDARKEHQ
Db	1	MSVDSKFNHGYHVSIGELETVLVHEPGREIDYITPARDELFFSAILESHDARKEHQ
QY	61	FVKIMDRGINVVELTDLVAETDYDLASKAAKEEFTEFETELTPVLTANKKAVRAFLS
Db	61	FVAELKANDINVVELLDVAETDYDLASKAAKEEFTEFETELTPVLTANKKAVRAFLS
QY	121	KPT-HMWFMMSGTKYBELGVESNELVIDMPNLTYTRDPFASVNGVTIHPMYIVR
Db	121	KXTSRELVINMAGITKYDELADHELIVDPMPNLTYTRDPFASVNGVTIHPMYIVR

Db 1 MSVDSKFGIHYVSEIGLESLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60  
QY 61 FVKIMKDRGINVVELTDLVAETVDLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLS 120  
Db 61 FVAELKANDINVELIDLVAETVDLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLS 120  
QY 121 KPT-HEMVPMGSIKYBELGVSENELIVDMPNLYFTRDPPASVGVNGVTIHFMYIYVR 179  
Db 121 KTSRLVIMMAGITKYDLGIEADHELIVDMPNLYFTRDPPASVGVNGVTIHFMYIYVR 180  
QY 180 RRETLFARFVRNHPKLVKTPWYDPAKMPLEGDVFIYNNETLVVGVSERTDLDITIL 239  
Db 181 QRETLFARFVRNHPKLVKTPWYDPAKMPLEGDVFIYNNETLVVGVSERTDLDITIL 240  
QY 240 LAKNIKANKEVEFKRIVAINVVKWTNLMHLDLTLTMDKDKFLYSPVANDVFKFWDYDLV 299  
Db 241 LAKNIKANKEVEFKRIVAINVVKWTNLMHLDLTLTMDKDKFLYSPVANDVFKFWDYDLV 300  
QY 300 NGGAEPQPLNGPLDKLILASIIKKEPVLIPIGAGATEMEIARETNFDCGTNYLAIKPGL 359  
Db 301 NGGAEPQPLNGPLDKLILASIIKKEPVLIPIGAGATEMEIARETNFDCGTNYLAIRPGV 360  
QY 360 VIGYDRNEKTNAAKAGITVLPFHGNQSLGNGNARCMSPLSRKDVK 408  
Db 361 VIGYDRNEKTNAAKAGITVLPFHGNQSLGNGNARCMSPLSRKDVK 409

RESULT 12  
AAR24528 standard; protein; 409 AA.  
XX AC AAR24528;  
XX DT 25-NOV-1992 (first entry)  
XX DE Arginine deiminase.  
XX KW AD; PEG.  
XX OS Mycoplasma arginini.  
XX PN JP04121187-A.  
XX PD 22-APR-1992.  
XX PF 10-SEP-1990; 90JP-00239387.  
XX PR 10-SEP-1990; 90JP-00239387.  
XX PA (NIHA ) NIPPON MINING CO.  
XX DR WPI; 1992-188063/23.  
XX DR N-PSDB; AAQ25395.  
XX PT Polyethylene glycol modified arginine deaminase prepn. - by covalently  
XX bonding arginine deiminase and ethylene glycol, useful as anticancer  
XX drug.  
XX PS Disclosure; Fig 1; 16pp; Japanese.  
XX CC The sequence given is arginine deiminase (AD) which, within the scope of  
XX the invention is modified by polyethylene glycol (PEG). This modification  
XX is caused by covalently bonding AD with PEG or its derivatives. This  
XX modified compound has equal anticancer effect to AD, but the blood  
XX stability is raised and the antigenicity is reduced. This product has  
XX low toxicity  
XX Sequence 409 AA;  
Query Match 81.8%; Score 1733.5; DB 2; Length 409;  
Best Local Similarity 80.7%; Pred. No. 1.3e-156;  
Matches 330; Conservative 40; Mismatches 38; Indels 1; Gaps 1;

QY 2 SVFDSKFGIHYVSEIGLESLVHEPGREIDYITPARLDELLFSAILESHDARKEHQSF 61  
Db 1 SVFDSKFGIHYVSEIGLESLVHEPGREIDYITPARLDELLFSAILESHDARKEHQSF 60  
QY 62 VKIMKDRGINVVELTDLVAETVDLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLSK 121  
Db 61 FVAELKANDINVELIDLVAETVDLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLSK 120  
QY 122 PT-HEMVPMGSIKYBELGVSENELIVDMPNLYFTRDPPASVGVNGVTIHFMYIYVR 180  
Db 121 KTSRLVIMMAGITKYDLGIEADHELIVDMPNLYFTRDPPASVGVNGVTIHFMYIYVR 180  
QY 181 RRETLFARFVRNHPKLVKTPWYDPAKMPLEGDVFIYNNETLVVGVSERTDLDITIL 240  
Db 181 QRETLFARFVRNHPKLVKTPWYDPAKMPLEGDVFIYNNETLVVGVSERTDLDITIL 240  
QY 241 LAKNIKANKEVEFKRIVAINVVKWTNLMHLDLTLTMDKDKFLYSPVANDVFKFWDYDLV 300  
Db 241 LAKNIKANKEVEFKRIVAINVVKWTNLMHLDLTLTMDKDKFLYSPVANDVFKFWDYDLV 300  
QY 301 NGGAEPQPLNGPLDKLILASIIKKEPVLIPIGAGATEMEIARETNFDCGTNYLAIKPGLV 360  
Db 301 NGGAEPQPLNGPLDKLILASIIKKEPVLIPIGAGATEMEIARETNFDCGTNYLAIRPGV 360  
QY 361 VIGYDRNEKTNAAKAGITVLPFHGNQSLGNGNARCMSPLSRKDVK 409  
Db 361 VIGYDRNEKTNAAKAGITVLPFHGNQSLGNGNARCMSPLSRKDVK 409  
RESULT 13  
AAR65454  
ID AAR65454 standard; protein; 410 AA.  
XX AC AAR65454;  
XX DT 19-NOV-1998 (first entry)  
XX DE Arginine deiminase (ADI) amino acid sequence.  
XX KW Arginine; ADI; recombinant; tumour; cancer; nitric oxide;  
XX KW nitric oxide synthase.  
XX OS Mycoplasma arthritis.  
XX PN WO9833519-A1.  
XX PD 06-AUG-1998.  
XX PF 27-JAN-1998; 98WO-US001635.  
XX PR 31-JAN-1997; 97US-00792283.  
XX PA (ENZO-) ENZON INC.  
XX PI Filpula DR, Wang M;  
XX DR WPI; 1998-437174/37.  
XX DR N-PSDB; AAV07550.  
XX PT Nucleic acid encoding arginine deiminase of Mycoplasma arthritis -  
XX useful for, e.g. treating tumours, cancers and nitric oxide-related  
XX conditions.  
XX PS Claim 1; Page 33-34; 54pp; English.  
XX CC This present sequence produces an arginine deiminase protein (ADI), an  
XX enzyme that hydrolyses arginine. To obtain the ADI nucleic acid, the M.  
XX arthritis strain 14152 was isolated from the american type culture  
XX collection, where from the arginine deiminase gene could be identified by  
XX the use of standard techniques. The protein encoded by this gene can be  
XX produced recombinantly as well as naturally to treat ADI-susceptible  
XX conditions, particularly tumours and cancers, or nitric oxide-related



CC conditions that require modulation of nitric oxide synthase. It can also  
CC modulate the adverse effects of a low protein diet  
XX  
SQ Sequence 410 AA;

Query Match 81.7%; Score 1732.5; DB 2; Length 410;  
Best Local Similarity 80.5%; Pred. No. 1.6e-156;  
Matches 330; Conservative 38; Mismatches 41; Indels 1; Gaps 1;

Qy 1 MSVPDSKFNHGVSEIGELTVLVHPEGRKEIDYITPARDELLEFSAILESHDARKEHQS 60  
Db 1 MSVPDSKFNHGVSEIGELTVLVHPEGRKEIDYITPARDELLEFSAILESHDARKEHKE 60  
Qy 61 FVKIMKRGINNVVELTDLVAETVYDLASKAAKEEFIEFTFLEETVPVLTEANKKAVRAFLLS 120  
Db 61 FVAELKRGINNVVELDLIVETVYDLASKAAKEELKEEFLLDSVPVLSDEHRAIVKKEFQS 120  
Qy 121 -KPTHEVMVFMMGGITKYELGVSENELIVDPMNLYFTTRDPPFASVGVNGVTIHFMYIVR 179  
Db 121 QKSTRSLVETMIAGITKHLKESDLELIIVDPMNLYFTTRDPPFASVGVNGVTIHFMYKVR 180  
Qy 180 RRETLPARFVRNHPKLVKTPWYDPAKMPKEGGVFIYNNETLVVGVSERTDLDITIL 239  
Db 181 QRETLPARFVRNHPKLVKTPWYDPAKMPKEGGVFIYNNETLVVGVSERTDLDITIL 240  
Qy 240 LAKNIKANKKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVFKFWDYDLV 299  
Db 241 LAKNIKANKKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVFKFWDYDLV 300  
Qy 300 NGGAEPQPLNGPLDPLDKLASIINKPEVLIPIGGAGATEMEIARETNFDGNTNLAIKPGL 359  
Db 301 NGGDAEPQPLNGPLDPLDKLASIINKPEVLIPIAGAGASQIDIERETHFDGNTNLAIVAPGI 360  
Qy 360 VIGYDRNEKNTNAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409  
Db 361 VIGYARNEKNTNAALKAAGITVLPFRGNQLSLGMGNARCMSPLSRKDVKW 410

RESULT 14  
AAR05713  
ID AAR05713 standard; protein; 405 AA.  
XX  
AC AAR05713;  
XX  
DT 25-MAR-2003 (revised)  
DT 10-MAR-2003 (revised)  
DT 16-AUG-1990 (first entry)  
XX  
DE Arginine deaminase.  
XX  
KW Arginine deaminase; carcinostatic; cancer; ds.  
XX  
OS Unidentified.  
XX  
PN JP02053490-A.  
XX  
PD 22-FEB-1990.  
XX  
PF 16-AUG-1988; 88JP-00202759.  
XX  
PR 16-AUG-1988; 88JP-00202759.  
XX  
PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.  
XX  
DR WPI; 1990-103119/14.  
DR N-PSDB; AAQ03739.  
XX  
PT Arginine de:iminase gene - where DNA contains base sequence that codes  
PT aminoacid sequence of arginine de:iminase composing polypeptide.  
XX  
PS Disclosure; Fig 1; 18pp; Japanese.  
XX  
CC Expression vector transformed by the gene may be used to produce large

CC quantities of arginine deaminase, useful as a carcinostatic. (Updated on  
CC 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct  
CC PA field.)  
XX  
SQ Sequence 405 AA;

Query Match 77.0%; Score 1632.5; DB 2; Length 405;  
Best Local Similarity 78.0%; Pred. No. 5.7e-147;  
Matches 319; Conservative 44; Mismatches 41; Indels 5; Gaps 5;

Qy 2 SVFDSKFNHGVSEIGELTVLVHPEGRKEIDYITPARDELLEFSAILESHDARKEHQS 61  
Db 1 SVFDSKFNHGVSEIGELTVLVHPEGRKEIDYITPARDELLEFSAILESTDAKEHKE 60  
Qy 62 VKIMKRGINNVVELTDLVAETVYDLASKAAKEEFIEFTFLEETVPVLTEANKKAVRAFLLS- 120  
Db 61 VELKKGGINNVVELDLIVETVYDLVVKTKQEKLLKDFLDDSEVPLSQKAVEKFLKSL 120  
Qy 121 KPTHEVMVFMMGGITKYELGVSENELIVDPMNLYFTTRDPPFASVGVNGVTIHFMYIVR 180  
Db 121 KSTKELIQYMMGGITKYDLGIKADKELIVDPMKLYFTTRDPPFASVGVNGVTIHFMYKVRQ 180  
Qy 181 RETLPARFVRNHPKLVKTPWYDPAKMPKEGGVFIYNNETLVVGVSERTDLDITIL 240  
Db 181 RETLPKSFITNHPKLVKTP-YYDPAKMLSEGGDVFIYNNDTLVVGVSERTDLETITLL 239  
Qy 241 AKNIKANKKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVFKFWDYDLVN 300  
Db 240 AKNIKANKKEVEFKRIIVAINVPK--TNLMHLDT--UTMLDKOKFLYSPIANDVFKF--DYDLVN 296  
Qy 301 GGAEPOPQPLNGPLDPLDKLASIINKPEVLIPIGGAGATEMEIARETNFDGNTNLAIKPGLV 360  
Db 297 GGSNPEVVGPLDPLDKLESIIINKPEVLIPIAGKATEIETA VETHFDGNTNLAIKPGLV 356  
Qy 361 IGYDRNEKNTNAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409  
Db 357 VGYSRVNKTNAALKAANGIKVLPFGNQLSLGMGNARCMSPLSRKDVKW 405

RESULT 15  
AAR20500  
ID AAR20500 standard; protein; 264 AA.  
XX  
AC AAR20500;  
XX  
DT 25-MAR-2003 (revised)  
DT 24-APR-1992 (first entry)  
XX  
DE Cell growth inhibiting peptide.  
XX  
KW Cancer.  
XX  
OS Mycoplasma arginini.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..8 /label= N-terminal peptide  
FT Peptide 31..38 /label= tryptic  
FT Peptide /notes= "B"  
FT Peptide 60..65 /label= tryptic  
FT Peptide /notes= "C"  
FT Peptide 138..145 /label= tryptic  
FT Peptide /notes= "F"  
FT Peptide 161..164 /label= tryptic  
FT Peptide /notes= "E"  
FT Peptide 189..195 /label= tryptic  
FT Peptide /notes= "A"  
FT Peptide 197..209

```
FT /label= tryptic
FT /note= "D"
FT Peptide 294..300
FT /label= tryptic
FT /note= "G"
XX
PN JF03284699-A.
XX
XX 16-DEC-1991.
XX
XX 12-APR-1990; 90JP-00097265.
XX
XX 09-FEB-1990; 90JP-00029975.
XX
XX (MOCH ) MOCHIDA PHARM CO LTD.
PA (HAYB ) HAYASHIBARA BIOCHEMICAL LAB.
XX
XX WPI; 1992-037730/05.
DR N-PSDB; AAQ20239.
XX
XX Protein obtd. from mycoplasma arginine, inhibiting cell growth - used as
PT immunosuppressant in organ transplant, as allergy suppressant and
PT treating auto-immune disease and malignant tumours.
XX
XX Claim 1; Fig 4; 20pp; Japanese.
XX
XX The protein is a novel growth inhibitor and can be used for various
CC treatments involving the suppression of cell growth. Tryptic peptide "B"
CC was used to design probes (see AAQ22582, 82 and 84) for the cloning of
CC the gene encoding the protein (see AAQ20239). (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
XX SQ Sequence 264 AA;

Query Match 51.0%; Score 1081.5; DB 2; Length 264;
Best Local Similarity 78.8%; Pred. No. 1.4e-94;
Matches 208; Conservative 28; Mismatches 27; Indels 1; Gaps 1;

Qy 1 MSVFDSKFNGLHYVSEIGELETVLVHEPFGREIDYITPARLDELFSAILSHDARKEHQ 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MSVFDSKFKGIHVYSEIGELESVLVHEPFGREIDYITPARLDELFSAILSHDARKEHQ 60
Qy ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEPIETFLETPVLTANKKAVRAFLS 120
Db ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 FVAELKANDINVVELIDLVAETDYLASQEAQKLIIEFLEDSFVLSEHKVVRNFKA 120
Qy 121 KPT-HEMVEFMMSGITKYELGVSENELIVDPMNLYFTTRDPPFASVNGVGTIHFMYIVR 179
Db ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 KKTSRKLVEIMMAGITKYDLGIEADHELIVDPMNLYFTTRDPPFASVNGVGTIHYMYKVR 180
Qy 180 RRETLFARFVRNHPKLVKTPMYVDPAKMPDIEGGDVFIYNNETLVGVSVERTDLDITL 239
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 QRETLFGRFVFSNHPKLVINTPWYDPSLKUSIEGGDVFIYNNETLVGVSVERTDLDITL 240
Qy 240 LAKNIKANKEVEFKRIVAINVPKW 263
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
241 LAKNIVANKECEFKRIVAINVPKW 264
```

Search completed: November 23, 2004, 15:47:50  
Job time : 161 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2004, 15:34:27 ; Search time 192 Seconds  
(without alignments)  
1225.668 Million cell updates/sec

Title: US-10-674-666-1

Perfect score: 2120

Sequence: 1 MSVDFSKFNGIHVYSEIGEL.....LGMGNARCMPLSRKDKVKW 409

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2115	99.8	408	1	ARCA MYCHO
2	1763.5	83.2	409	1	ARCA MYCAR
3	1721.5	81.2	409	2	Q9RND4
4	1169.5	55.2	452	2	Q8EYF6
5	1103	52.0	408	2	Q7NBF0
6	1057	49.9	404	1	ARCA MYCPN
7	986	46.5	409	2	Q6KI67
8	986	46.5	409	2	AAT27709
9	708.5	33.4	410	2	Q6HP29
10	707.5	33.4	410	2	Q811I1
11	705.5	33.3	410	2	Q73E87
12	705.5	33.3	410	2	AAS39407
13	688	32.5	403	2	Q8KZ88
14	682.5	32.2	409	2	Q8GG81
15	681.5	32.1	413	1	ARCA BACL1
16	679	32.0	410	1	ARCA_STRPY
17	678.5	32.0	410	2	Q8DWQ2
18	678.5	32.0	410	2	Q8E2K0
19	677	31.9	410	1	ARCA STRP3
20	672	31.7	411	2	Q6TK74
21	672	31.7	411	2	AAR30322
22	670.5	31.6	408	2	Q93K67
23	660	31.1	413	1	ARCA CLOPE
24	655.5	30.9	409	2	Q9KJG1
25	651.5	30.7	409	1	ARCA STRPN
26	650	30.7	410	2	Q8GND5
27	648.5	30.6	411	2	Q6GG7
28	644.5	30.4	411	1	ARCA_STAAN
29	644.5	30.4	411	2	Q7AS72
30	644.5	30.4	411	2	Q6GG39
31	644.5	30.4	411	2	CAD98181

32	641.5	30.3	411	1	ARCA_STAEP	Q8CG95 staphylococ
33	640.5	30.2	411	1	ARCA STAAM	Q99r02 staphylococ
34	638.5	30.1	410	1	ARCA LACLC	Q9k576 lactococcus
35	638.5	30.1	410	2	Q9KGV5	Q9k576 lactococcus
36	638	30.1	408	1	ARCA LISIN	Q92fr7 listeria in
37	632	29.8	410	1	ARCA_LISMO	Q8ya60 listeria mo
38	631.5	29.8	410	1	ARCA LACLA	P58013 lactococcus
39	631	29.8	410	2	Q725C1	Q725c1 listeria mo
40	631	29.8	410	2	AAT02840	Aat02840 listeria
41	625	29.5	409	1	ARCA LACSK	O53088 lactobacill
42	624.5	29.5	410	2	Q73QJ2	Q73qj2 treponena d
43	624.5	29.5	410	2	AAS10946	Aas10946 treponema
44	624.5	29.5	468	2	Q8RDD8	Q8rdd8 thermoanaer
45	617.5	29.1	415	2	Q8VW56	Q8vww56 oenococcus

ALIGNMENTS

RESULT 1					
ARCA_MYCHO STANDARD; PRT; 408 AA.					
AC	P41141				
DT	01-FEB-1995 (Rel. 31, Created)				
DT	01-FEB-1995 (Rel. 31, Last sequence update)				
DT	05-JUL-2004 (Rel. 44, Last annotation update)				
DE	Arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD) .				
GN	Namesarca;				
OS	Mycoplasma hominis.				
OC	Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.				
OX	NCBI_TaxID=2098;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=92396053; PubMed=1522817;				
RA	Harasawa R., Koshimizu K., Kitagawa M., Asada K., Kato I.;				
RT	"Nucleotide sequence of the arginine deiminase gene of Mycoplasma hominis.";				
RL	Microbiol. Immunol. 36:661-665(1992) .				
CC	- - CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3) .				
CC	- - PATHWAY: Arginine degradation via arginine deiminase; first step.				
CC	- - SUBCELLULAR LOCATION: Cytoplasmic (Potential).				
CC	- - SIMILARITY: Belongs to the arginine deiminase family.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; D13314; BAA02571.1; --				
DR	HAWAP; MF_00242; --; 1.				
DR	InterPro; IPR003198; Amidino trans.				
DR	InterPro; IPR003876; Arg deiminase.				
DR	Pfam; PF02274; Amidinotransf; 1.				
DR	PRINTS; PR01466; ARGDEIMINASE.				
DR	TIGRFAMs; TIGR01078; arca; 1.				
KW	Arginine metabolism; Hydrolase.				
FT	INIT MET 0 By similarity.				
FT	ACT_SITE 396 396 Amidino-cysteine intermediate (By similarity).				
FT	ACT_SITE 396 396				
SQ	SEQUENCE 408 AA; 46182 MW; 53A11D6373DBBE93 CRC64;				
Query Match 99.8%; Score 2115; DB 1; Length 408;					
Best Local Similarity 100.0%; Pred. No. 4.2e-136;					
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	2	SVFDSKFNHIVYSEIGELTVLHPGRIEYITPARDELIFSAILSHDARKEHQSF	61		
DB	1	SVFDSKFNHIVYSEIGELTVLHPGRIEYITPARDELIFSAILSHDARKEHQSF	60		
QY	62	VKIMDRGINVVELTDLVAETVDLASKAAKEEPIETFLEETVPVLTANKKAVRAFLSK	121		

Db 61 VKMKDGINVVELTDLVAETVYDLASKAAKEEFTETLEEVFVLTETANKKAVRAFLSK 120  
Qy 122 PTHEMVFMSGITYKELGVSENELIVDPMPNLYFTRDPPASVGVNGVTIHFMYIYVRR 181  
Db 121 PTHEMVFMSGITYKELGVSENELIVDPMPNLYFTRDPPASVGVNGVTIHFMYIYVRR 180  
Qy 182 ETLFARFVRNHPKLVKTPWYDPAKMPLEGDVFYNNETLVVGVSERTDLDITLLA 241  
Db 181 ETLFARFVRNHPKLVKTPWYDPAKMPLEGDVFYNNETLVVGVSERTDLDITLLA 240  
Qy 242 KNIKANKEVEPKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPIANDVFKFWDYDLVNG 301  
Db 241 KNIKANKEVEPKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPIANDVFKFWDYDLVNG 300  
Qy 302 GAEPQOLNGLPLDKLASIINKEPVLIPIGGAGATEMEIARETNFDGTNYLAIKPGLVI 361  
Db 301 GAEPQOLNGLPLDKLASIINKEPVLIPIGGAGATEMEIARETNFDGTNYLAIKPGLVI 360  
Qy 362 GYDRNEKTNAAKKAAGITVLPFHGNQSLGNGNARCMSPLSRKDVKW 409  
Db 361 GYDRNEKTNAAKKAAGITVLPFHGNQSLGNGNARCMSPLSRKDVKW 408

RESULT 2  
ARCA MYCAR  
ID \_ARCA\_MYCAR STANDARD; PRT; 409 AA.  
AC P23793;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD).  
GN Name=arca;  
OS Mycoplasma arginini.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
OX NCBI\_TaxID=2094;  
RN [1]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC STRAIN=ATCC 23838;  
RX MEDLINE=94361803; PubMed=7765234;  
RA Misawa S., Aoshima M., Takaku H., Matsumoto M., Hayaashi H.;  
RT "High-level expression of Mycoplasma arginine deiminase in Escherichia  
RT coli and its efficient renaturation as an anti-tumor enzyme.";  
RL J. Biotechnol. 36:145-155 (1994).  
RN [2]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=91034196; PubMed=2228248;  
RA Ohno T., Ando O., Sugimura K., Taniat M., Suzuki M., Fukuda S.,  
RA Nagase Y., Yamamoto K., Azuma I.;  
RT "Cloning and nucleotide sequence of the gene encoding arginine  
RT deiminase of Mycoplasma arginini.";  
RL Infect. Immun. 58:3788-3795 (1990).  
RN [3]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX STRAIN=KM101;  
RC MEDLINE=90220524; PubMed=2325633;  
RA Kondo K., Sone H., Yoshida H., Toida T., Kanatani K., Hong Y.-M.,  
RA Nishino N., Tanaka J.-I.;  
RT "Cloning and sequence analysis of the arginine deiminase gene from  
RT Mycoplasma arginini.";  
RL Mol. Gen. Genet. 221:81-86 (1990).  
CC -!- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3).  
CC -!- PATHWAY: Arginine degradation via arginine deiminase; first step.  
CC -!- SUBUNIT: Homodimer.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
CC -!- SIMILARITY: Belongs to the arginine deiminase family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
CC  
CC EMBL; X54141; CAA38080.1; -;  
DR EMBL; X54312; CAA38210.1; -;  
DR EMBL; X52459; CAA36693.2; -;  
DR PIR; A41465; A41465.  
DR PDB; 1LXY; X-ray; A/B=1-409.  
DR HAMAP; MF\_00242; -; 1.  
DR InterPro; IPR003198; Amidino trans.  
DR InterPro; IPR003876; Arg deiminase.  
DR Pfam; PF02274; Amidinotransf. 1.  
DR PRINTS; PR01466; ARGDEIMINASE.  
DR TIGRFAMs; TIGR01078; arca; 1.  
KW 3D-structure; Arginine metabolism; Direct protein sequencing;  
KW Hydrolase.  
FT INIT MET 0 0  
FT ACT\_SITE 397 397 Amidino-cysteine intermediate (By  
FT similarity).  
FT CONFLICT 75 75 I -> T (in Ref. 3).  
FT CONFLICT 119 119 A -> S (in Ref. 3).  
FT CONFLICT 125 125 E -> K (in Ref. 2).  
FT CONFLICT 374 409 EAAGIKVLPFHGNQSLGNGNARCMSPLSRKDVKW -> D  
FT KKDYLRPISI (in Ref. 3).  
SQ SEQUENCE 409 AA; 46376 MW; 71EC4E8D7FB69D61 CRC64;  
Query Match 83.2%; Score 1763.5; DB 1; Length 409;  
Best Local Similarity 82.2%; Pred. No. 4.1e-112;  
Matches 336; Conservative 36; Mismatches 36; Indels 1; Gaps 1;  
Qy 2 SVFDSKFNHGVHYSEIGELTDLVAETVYDLASKAAKEEFTETLEEVFVLTETANKKAVRAFLSK 61  
Db 1 SVFDSKFNHGVHYSEIGELTDLVAETVYDLASKAAKEEFTETLEEVFVLTETANKKAVRAFLSK 60  
Qy 62 VKMKDGINVVELTDLVAETVYDLASKAAKEEFTETLEEVFVLTETANKKAVRAFLSK 121  
Db 61 VAEKANDINNVVELIDLVAETVYDLASKAAKEEFTETLEEVFVLTETANKKAVRAFLSK 120  
Qy 122 PT-HEMVFMSGITYKELGVSENELIVDPMPNLYFTRDPPASVGVNGVTIHFMYIYVRR 180  
Db 121 KTSRELVEIMMAGITKYDLGIEADHDLIVDPMPNLYFTRDPPASVGVNGVTIHFMYIYVRR 180  
Qy 181 RETLFAFVRNHPKLVKTPWYDPAKMPLEGDVFYNNETLVVGVSERTDLDITLL 240  
Db 181 RETLFSRFVSNHPKLVKTPWYDPSLKLSIEGDFYNNETLVVGVSERTDLDITLL 240  
Qy 241 AKNIKANKEVEPKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPIANDVFKFWDYDLVNG 300  
Db 241 AKNIKANKEVEPKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPIANDVFKFWDYDLVNG 300  
Qy 301 GAEPQOLNGLPLDKLASIINKEPVLIPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
Db 301 GAEPQOLNGLPLDKLASIINKEPVLIPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
Qy 361 IGYDRNEKTNAAKKAAGITVLPFHGNQSLGNGNARCMSPLSRKDVKW 409  
Db 361 IGYDRNEKTNAAKKAAGITVLPFHGNQSLGNGNARCMSPLSRKDVKW 409

RESULT 3  
Q9RND4  
ID Q9RND4 PRELIMINARY; PRT; 409 AA.  
AC Q9RND4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Arginine deiminase.  
GN Name=arca;  
OS Mycoplasma arthritidis.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
OX NCBI\_TaxID=2111;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PG6;

```

RX MEDLINE=20353471; PubMed=10894746;
RA Dybvig K., French C.T., Voelker L.L.;
RT "Construction and use of derivatives of transposon Tn4001 that
function in Mycoplasma pulmonis and Mycoplasma arthritis.";
RL J. Bacteriol. 182:4343-4347(2000).
DR EMBL; AF182646; AAD55448.1; -.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0006527; P:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino trans.
DR InterPro; IPR003876; Arg deiminase.
DR Pfam; PF02274; Amidinotransf; 1.
DR PRINTS; PR01466; ARGDEIMINASE.
DR TIGRFAMs; TIGR01078; arca; 1.
SQ SEQUENCE 409 AA; 46039 MW; 7PEDC7F182BFF5C7 CRC64;

Query Match 81.2%; Score 1721.5; DB 2; Length 409;
Best Local Similarity 80.4%; Pred. No. 3.1e-109; Indels 1; Gaps 1;
Matches 329; Conservative 38; Mismatches 41;

Qy 1 MSVDSKFNFGIHVYSEIGELETVLVHPGREGIDYITPARLDELLFSAILESHDARKEHQS 60
Db 1 MSVDSKFKGIHVYSEIGELETVLVHPGREGIDYITPARLDELLFSAILESHDARKEHE 60

Qy 61 FVKIMKDRGINVELTDLVAETYDLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLS 120
Db 61 FVAKELKRGINVELVDLIYETVYDLASKAAKEKLEEFLLDSDAPVLSDEHRAAVKKFLQS 120

Qy 121 -KPTHEMVEFMMSGITKYELGVSENELIVDPMPNLYFTTRDPFASVNGVGTIHFMYIVR 179
Db 121 QKSTRSLVSEYIMAGITKHDLDKLSDELIVDPMPNLYFTTRDPFASVNGVGTIHFMYKVR 180

Qy 180 RRETLFARFVRNHPKLVKTPWYDPAKMPPIEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 QRETLFSRFVSNHPKLVNTPWYDPAEGLSIEGGDVFIYNNETLVVGVSERTDLDITL 240

Qy 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDLTLMDKNKFLYSPINDVFKFWDYDLV 299
Db 241 LAKNIKANKECEFKRIVAINVPKWTNLMHLDLTLMDKNKFLYSPINDVFKFWDYDLV 300

Qy 300 NGGAEPQPLNGPLDLKLASIINKEPVLPIPGAGATEMEIARETNDFTNLAIKPGL 359
Db 301 NGGDAPOVNGPLNGPLDLKLASIIGKFTLPIAGAGASQIDIERETHFDGNTYLAAPGI 360

Qy 360 VIGYDRNEKTNALKAAGITVLPHGNQLSLGNARCMSPLSRKDKVK 408
Db 361 VIGYARNEKTNALKAAGITVLPHGNQLSLGNARCMSPLSRKDKVK 409

RESULT 4
Q8EVF6 PRELIMINARY; PRT; 452 AA.
AC Q8EVF6
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Arginine deiminase.
GN OrderedLocusNames=MYPB6080;
OS Mycoplasma penetrans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=28227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HF-2;
RX MEDLINE=22354719; PubMed=12466555;
RA Sasaki Y., Ishikawa J., Yamaehira A., Oshima K., Kenri T., Furuya K.,
RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
RT "The complete genomic sequence of Mycoplasma penetrans, an
RT intracellular bacterial pathogen in humans.";
RL Nucleic Acids Res. 30:5293-5300(2002).
DR EMBL; AP004172; BAC44398.1; -.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0006527; P:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino trans.

MEDLINE=20353471; PubMed=10894746;
RA Dybvig K., French C.T., Voelker L.L.;
RT "Construction and use of derivatives of transposon Tn4001 that
function in Mycoplasma pulmonis and Mycoplasma arthritis.";
RL J. Bacteriol. 182:4343-4347(2000).
DR EMBL; AF182646; AAD55448.1; -.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0006527; P:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino trans.
DR InterPro; IPR003876; Arg deiminase.
DR Pfam; PF02274; Amidinotransf; 1.
DR PRINTS; PR01466; ARGDEIMINASE.
DR TIGRFAMs; TIGR01078; arca; 1.
SQ SEQUENCE 409 AA; 46039 MW; 7PEDC7F182BFF5C7 CRC64;

Query Match 81.2%; Score 1721.5; DB 2; Length 409;
Best Local Similarity 80.4%; Pred. No. 3.1e-109; Indels 1; Gaps 1;
Matches 329; Conservative 38; Mismatches 41;

Qy 1 MSVDSKFNFGIHVYSEIGELETVLVHPGREGIDYITPARLDELLFSAILESHDARKEHQS 60
Db 1 MSVDSKFKGIHVYSEIGELETVLVHPGREGIDYITPARLDELLFSAILESHDARKEHE 60

Qy 61 FVKIMKDRGINVELTDLVAETYDLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLS 120
Db 61 FVAKELKRGINVELVDLIYETVYDLASKAAKEKLEEFLLDSDAPVLSDEHRAAVKKFLQS 120

Qy 121 -KPTHEMVEFMMSGITKYELGVSENELIVDPMPNLYFTTRDPFASVNGVGTIHFMYIVR 179
Db 121 QKSTRSLVSEYIMAGITKHDLDKLSDELIVDPMPNLYFTTRDPFASVNGVGTIHFMYKVR 180

Qy 180 RRETLFARFVRNHPKLVKTPWYDPAKMPPIEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 QRETLFSRFVSNHPKLVNTPWYDPAEGLSIEGGDVFIYNNETLVVGVSERTDLDITL 240

Qy 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDLTLMDKNKFLYSPINDVFKFWDYDLV 299
Db 241 LAKNIKANKECEFKRIVAINVPKWTNLMHLDLTLMDKNKFLYSPINDVFKFWDYDLV 300

Qy 300 NGGAEPQPLNGPLDLKLASIINKEPVLPIPGAGATEMEIARETNDFTNLAIKPGL 359
Db 301 NGGDAPOVNGPLNGPLDLKLASIIGKFTLPIAGAGASQIDIERETHFDGNTYLAAPGI 360

Qy 360 VIGYDRNEKTNALKAAGITVLPHGNQLSLGNARCMSPLSRKDKVK 408
Db 361 VIGYARNEKTNALKAAGITVLPHGNQLSLGNARCMSPLSRKDKVK 409

RESULT 5
Q7NBF0 PRELIMINARY; PRT; 408 AA.
AC Q7NBF0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Arca (EC 3.5.3.6).
GN Name=arca; OrderedLocusNames=MYCGA3290; ORFNames=MGA_1220;
OS Mycoplasma gallisepticum.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=22830409; PubMed=12949158;
RA Papazisi L., Gorton T.S., Kutieh G., Markham P.F., Browning G.F.,
RA Nguyen D.K., Swartzell S., Madan A., Mahairas G., Geary S.J.;
RT "The complete genome sequence of the avian pathogen Mycoplasma
RT gallisepticum strain R(low).";
RL Microbiology 149:2307-2316(2003).
DR EMBL; AB016968; AAP56679.1; -.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006527; P:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino trans.
DR InterPro; IPR003876; Arg deiminase.
DR Pfam; PF02274; Amidinotransf; 1.
DR PRINTS; PR01466; ARGDEIMINASE.
DR Complete proteome; Hydrolase.
SQ SEQUENCE 408 AA; 47084 MW; 36EC0BF5A6A8F58A CRC64;

Query Match 52.0%; Score 1103; DB 2; Length 408;
Best Local Similarity 52.2%; Pred. No. 4.9e-67;

```





```

QY 180 RRETLFARFVRNHPKLVK--TPWYDPAKMPKEGGDFVYNNETLVVGVSERTDLDTI 237
DB 181 RRESLFMEYIIKYHPRFAKHNVPIWLDKDYKFFIEGGDELINETAIGVSARTSAKA 240
QY 238 TLLAKNIKANKEVEFKRIVAINVPKWTNMLHDLTWLMDKNKFLYSPANDVFKFWYD 297
DB 241 ERLAKNL-FSRQNKIKKVLAIETPKRAFMEHLDVFTVMDVYDKFTIHPAIQGPKNMNIY 299
QY 298 LVNGAEPQPOQ--LNGPLDKLLASIIIN-KEPVLPIGGAGATETARETNFGTNYLA 354
DB 300 ILEKGSDEETLKITHRTSLMEALKEVLSELVIFPCGGGDV--IASAREQWNGSNTLA 357
QY 355 IKPGLVIGYDRNEKTNAAKAGITVLPFHGNQSLGGMNARCMSPKSRKDV 407
DB 358 IAPGVVVYDRNYVNTLLREHGIEVIELSSLSRGRGPRCWSMPIVRKDI 410

RESULT 10
Q81111 ID Q81111 PRELIMINARY; PRT; 410 AA.
AC Q81111;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Arginine deiminase (EC 3.5.3.6).
GN ORFNames=BC0406;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Wazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Fusch G., Haseil Korn R., Fongstein M., Ehrlich S.D.,
RA Overbeek R., Kyrides N.C.
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
DR EMBL: AE016999; AAP07446.1; -
DR GO: GO:0016990; F:arginine deiminase activity; IEA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0006527; P:arginine catabolism; IEA.
DR InterPro: IPR003198; Amidino trans.
DR InterPro: IPR003876; Arg deiminase.
DR Pfam: PF02274; Amidinotransf. 1.
DR PRINTS: PR01466; ARGDEIMINASE.
DR TIGRFAMs: TIGR01078; arca; 1.
KW Hydrolase.
SQ SEQUENCE 410 AA; 46880 MW; 3D3AE8489168BD73 CRC64;

Query Match 33.4%; Score 707.5; DB 2; Length 410;
Best Local Similarity 40.9%; Pred. No. 4.9e-40;
Matches 169; Conservative 70; Mismatches 151; Indels 23; Gaps 10;

QY 11 IHVYSEIGELTVLVEHPGREGIDYITPARDELFFSAILSHDARKEHQSFVKIMKDRGI 70
DB 5 IHVTSEIGELQTVLLKRPKEVENITPDYLOQLLFDIDPILPIIQKEDHYFAQTLLNRGV 64
QY 71 NVVELTDLVAETDYLAKAAKEEFIEFTLEETVPVLTEANKKAVRAFLSKPHEMVEFM 130
DB 65 EVLYLEKLAEEA--LVDDKLRREFVDRILKEGQADVNAH-QTLKEYLLSFSNEELIQKI 121
QY 131 MSGITK-----YELGVSENELIVDPNLYFTDRDPASVGVGTTHFMFYIVR 179
DB 122 MGVGRKNEIETSKTHLYEL-MEDHYPFYLDPMPLNYFTRDPAASVGDGLTINKREPAR 180
QY 180 RRETLFARFVRNHPKLVK--TPWYDPAKMPKEGGDFVYNNETLVVGVSERTDLDTI 237
DB 181 RRESLFMEYIIKYHPRFAKHNVPIWLDKDYKFFIEGGDELINETAIGVSARTSAKA 240
QY 238 TLLAKNIKANKEVEFKRIVAINVPKWTNMLHDLTWLMDKNKFLYSP- IANDVFKFWYD 296
DB 241 RRESLFMEYIIKYHPRFAKHNVPIWLDKDYKFFIEGGDELINETAIGVSARTSAKA 299
QY 297 LVNGAEPQPOQ--LNGPLDKLLASIIIN-KEPVLPIGGAGATETARETNFGTNYLA 354
DB 300 ILEKGSDEETLKITHRTSLMEALKEVLSELVIFPCGGGDV--IASAREQWNGSNTLA 357

```

```

DB 241 ERLAKNL-FSRQNKIKKVLAIETPKRAFMEHLDVFTVMDVYDKFTIHPAIQGPKNMNIY 299
QY 297 LVNGAEPQPOQ--LNGPLDKLLASIIIN-KEPVLPIGGAGATETARETNFGTNYLA 354
DB 300 ILEKGSDEETLKITHRTSLMEALKEVLSELVIFPCGGGDV--IASAREQWNGSNTLA 357
QY 355 IKPGLVIGYDRNEKTNAAKAGITVLPFHGNQSLGGMNARCMSPKSRKDV 407
DB 358 IAPGVVVYDRNYVNTLLREHGIEVIELSSLSRGRGPRCWSMPIVRKDI 410

RESULT 11
Q73E87 ID Q73E87 PRELIMINARY; PRT; 410 AA.
AC Q73E87;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Arginine deiminase (EC 3.5.3.6).
GN Name=archa; Ordered locus Names=BCE0472;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pX01.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL: AS017265; AAS39407.1; -
DR TIGR: BCE0472; -
DR GO: GO:0016990; F:arginine deiminase activity; IEA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR InterPro: IPR003198; Amidino trans.
DR InterPro: IPR003876; Arg deiminase.
DR Pfam: PF02274; Amidinotransf. 1.
DR PRINTS: PR01466; ARGDEIMINASE.
DR TIGRFAMs: TIGR01078; arca; 1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 410 AA; 46938 MW; 8D7846C8D206579A CRC64;

Query Match 33.3%; Score 705.5; DB 2; Length 410;
Best Local Similarity 40.9%; Pred. No. 6.7e-40;
Matches 169; Conservative 70; Mismatches 151; Indels 23; Gaps 10;

QY 11 IHVYSEIGELTVLVEHPGREGIDYITPARDELFFSAILSHDARKEHQSFVKIMKDRGI 70
DB 5 IHVTSEIGELQTVLLKRPKEVENITPDYLOQLLFDIDPILPIIQKEDHYFAQTLLNRGV 64
QY 71 NVVELTDLVAETDYLAKAAKEEFIEFTLEETVPVLTEANKKAVRAFLSKPHEMVEFM 130
DB 65 EVLYLEKLAEEA--LVDDKLRREFVDRILKEGQADVNAH-QTLKEYLLSFSNEELIQKI 121
QY 131 MSGITK-----YELGVSENELIVDPNLYFTDRDPASVGVGTTHFMFYIVR 179
DB 122 MGVGRKNEIETSKTHLYEL-MEDHYPFYLDPMPLNYFTRDPAASVGDGLTINKREPAR 180
QY 180 RRETLFARFVRNHPKLVK--TPWYDPAKMPKEGGDFVYNNETLVVGVSERTDLDTI 237
DB 181 RRESLFMEYIIKYHPRFAKHNVPIWLDKDYKFFIEGGDELINETAIGVSARTSAKA 240
QY 238 TLLAKNIKANKEVEFKRIVAINVPKWTNMLHDLTWLMDKNKFLYSP- IANDVFKFWYD 296
DB 241 ERLAKNL-FSRQNKIKKVLAIETPKRAFMEHLDVFTVMDVYDKFTIHPAIQGPKNMNIY 299
QY 297 LVNGAEPQPOQ--LNGPLDKLLASIIIN-KEPVLPIGGAGATETARETNFGTNYLA 354
DB 300 ILEKGSDEETLKITHRTSLMEALKEVLSELVIFPCGGGDV--IASAREQWNGSNTLA 357

```



```

QY 355 IKPGLVIGYDRNEKTNAAKAGITVLPFHGNOLSLGNGNARCMWSMPLSRKDV 407
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 358 IAPGVVVTYDRNVSTNLLREHGIEVIEVLSSELSSRGRGRCMSPVIRKDI 410
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :

RESULT 12
AAS39407 PRELIMINARY; PRT; 410 AA.
AC AAS39407;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 04-MAY-2004 (T-EMBLrel. 27, Last annotation update)
DE Arginine deiminase (EC 3.5.3.6).
GN ARCA OR BCE0472.
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.B., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolisoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXOI.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AS017265; AAS39407.1; -.
DR TIGR; BCE0472; -.
KW Hydrolase.
SQ SEQUENCE 410 AA; 46938 MW; 8D7846C8D026579A CRC64;

Query Match 33.3%; Score 705.5; DB 2; Length 410;
Best Local Similarity 40.9%; Pred. No. 67e-40;
Matches 159; Conservative 70; Mismatches 151; Indels 23; Gaps 10;

QY 11 IHVYSIGELETVLVHEPGREIDYITPARLDELFSAILSHDARKEHOSFVKIMKDRGI 70
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 5 IHVTSIGELETVLVLRPGKEVENLTPDYLQQLFDDIPYLPITQKEHDYFAQTLRNGV 64
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :

QY 71 NVVELTDLVAETVDLASKAAKEFIETFLTEETVPVLTEANKKAVRAFLLSKPTHEMVE 130
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 65 EVLYLEKLAEEA--LVDDKLLREFFVDRIKKEGQADVNAH-QTLKSYLLSFSNEELIQKI 121
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :

QY 131 MSGITK-----YELGVSENELIVDPNPLYFTDRDPASVGVNGVTIHFMYIVR 179
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 122 MGVGRKNEIETSKTHLYEL-MEDHYFPYLDPMNLYFTDRDPASVGDGLTINKMREPAR 180
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :

QY 180 RRETLFARFVRNHPKLVK--TPWYYDPAMKPIEGGDVFIYNNETLVVGVSERTDLDTI 237
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 181 RRESLFEVIKYHPRFEKHNVPIWLDKDYKPIEGGDELILNEETIAGVSARTSAKAI 240
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :

QY 238 TLLAKNIKANKVEFEKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSP-IANDVPKFDY 296
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 241 ERLAKNL-FSRQNKIKVLAIEIPKCRAPMHLDTVFTMVDYDKFTIHPAIQGGKGNMNIY 299
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :

QY 297 DLVNGGAEPOL-NGLPDLKLASIN-KEPVLIPIGGAGATEMBIARETNFDGNTYLA 354
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 300 ILEKGSDEETLKITHRTSLMEALKEVIGSELVLIIFCGGVDV--IASAREQWNGSNTLA 357
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :

QY 355 IKPGLVIGYDRNEKTNAAKAGITVLPFHGNOLSLGNGNARCMWSMPLSRKDV 407
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 358 IAPGVVVTYDRNVSTNLLREHGIEVIEVLSSELSSRGRGRCMSPVIRKDI 410
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :

RESULT 13
Q8KZ88 PRELIMINARY; PRT; 403 AA.
AC Q8KZ88;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Arginine dihydrolase (EC 3.5.3.6).
GN Name=arCA;

```

```

OS Granulicatella elegans.
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Granulicatella
OX NCBI_TaxID=137732;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HHC5;
RA Sato S., Inoue M.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB091333; BAC11861.1; -.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006527; P:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino trans.
DR InterPro; IPR003876; Arg deiminase.
DR Pfam; PF02274; Amidinotransf; 1.
DR PRINTS; PR01466; ARGDEIMINASE.
DR TIGRFAMs; TIGR01078; arCA; 1.
KW Hydrolase.
SQ SEQUENCE 403 AA; 45437 MW; 0BA6C55314CF7844 CRC64;

Query Match 32.5%; Score 688; DB 2; Length 403;
Best Local Similarity 38.7%; Pred. No. 1e-38;
Matches 159; Conservative 73; Mismatches 157; Indels 22; Gaps 8;

QY 9 NGHVYSIGELETVLVHEPGREIDYITPARLDELFSAILSHDARKEHOSFVKIMKOR 68
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 3 NFIHVSEIGRLKKVCLHRPGKELENLMPDYLERLLFDDIPYLEDQAQKHDAAETLRNA 62
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :

QY 69 GINVELTDLVAETVDLASKAAKEFIETFLTEETVPVLTEANKKAVRAFLLSKPTHEMVE 128
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 63 GVEVLVLEQLAAEAIDAA--GVREEFVDEWLSE-AGVASVASQKAKEHLLSLPTDLVL 119
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :

QY 129 FMSGITKTKYELGV-----ESENELIVDPNPLYFTDRDPASVGVNGVTIHFMYIVR 179
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 120 KTMGEGRKTEVOAEATTLAGMYETDYPFVVDPMNLYFTDRDPATWANGVSLNHYADTR 179
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :

QY 180 RRETLFARFVRNHPKLV--VKTWPYYDPAMKPIEGGDVFIYNNETLVVGVSERTDLDTI 237
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 180 NRETIYCKIIFYHPYGVNGKVPFFYNNRTEDTRIEGGDELVLSEKVLAVGISORTDARSI 239
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :

QY 238 TLLAKNIKANKVEFEKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSP-IANDVPKFDY 297
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 240 EKLLKII---AETDFKQVLAFAVIGENKEMHLDTVFTHDYDKFTIHPETQGLKV--FS 294
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :

QY 298 LVNGGAEPOLNGLPDLKLASINKEPV-LIPIGGAGATEMBIARETNFDGNTYLAIK 356
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 295 ITKGENMVPYIELTDEKLENVLAKALGLPSVTLLIPCG--GGDPVAAAREQWNGSNTLITIA 352
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :

QY 357 PGLVIGYDRNEKTNAAKAGITVLPFHGNOLSLGNGNARCMWSMPLSRKDV 407
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 353 PGEVVVYDRNVVTNEILEKYGKIKHKGISELVGRGRCMSPPERENL 403
| | | | | : | | | : | | | : | | | : | | | : | | | : | | | :

RESULT 14
Q8GG81 PRELIMINARY; PRT; 409 AA.
AC Q8GG81;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Ads.
GN Name=adIs;
OS Streptococcus suis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1307;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=19841.1;
RA Winterhoff N.; Goethe R., Gruening P., Valentin-Weigand P.;
RT "Identification and Characterization of Two Temperature-induced
RT Surface-associated Proteins of Streptococcus suis with High Homologies

```

RT to Members of the Arginine Deiminase System of Streptococcus  
 RL J. Bacteriol. 0:0-0(2002).  
 DR EMBL: AF545864; AAN76306.1; --  
 DR GO: GO:0006990; P:arginine deiminase activity; IEA.  
 DR GO: GO:0006527; P:arginine catabolism; IEA.  
 DR InterPro: IPR003198; Arg deiminase.  
 DR InterPro: IPR003876; Arg deiminase.  
 DR Pfam: PF02274; Amidinotransf. 1.  
 DR PRINTS: PR01466; ARGDEIMINASE.  
 DR TIGRFAMs: TIGR01078; arcA, 1.  
 DR ACT\_SITE 402 402 Amidino-cysteine intermediate (By  
 FT similarity).  
 SQ SEQUENCE 409 AA; 46345 MW; 4DC04E37B40394C CRC64;

Query Match 32.2%; Score 682.5; DB 2; Length 409;  
 Best Local Similarity 39.4%; Pred. No. 2.5e-38;  
 Matches 164; Conservative 76; Mismatches 145; Indels 31; Gaps 12;  
 QY 11 IHVYSEIGLETVLVEHGREIDYITPARLDELFSAILSHDARKEHQSFVKIMKDRGI 70  
 Db 6 IHVFSIGLKKVLMHPRKGIENLMPDYLRLFFDDIPFLDPAQKEHDAFAQALRDEGV 65  
 QY 71 NVVELTDLVAETVDLASKAAKEEFTETLEETVPVLTANKKAVRAFLLS-KPTHEMVFP 129  
 Db 66 EVLYLEKLAES--LVTPREIQFTIDELEE-ANIRGRATKKAIRKULMSTEDNQELVEK 122  
 QY 130 MMSGITKYELG-----VESENELIVDPNLYFTTRDPFASVGVNGVTIHFMRVI 177  
 Db 123 TMAGVQKAEPLKIPSEBKGLTDLVSESYPPAIDPMPNLYFTTRDPFATIGNAVSLNHMYSE 182  
 QY 178 VRRRETLFARFVRNHPKL-VKTPWYDDPAMKPIEGDVFYINNETLVGVSVSRTDLD 236  
 Db 183 TRNRETLGKYIFTHHPYGGKPLVYNREETTRIEGGDELVLKSLVAVGISORTDAAS 242  
 QY 237 ITLLAKNIKANKVEFKRIVAINVPKTNLMHLDITLMLDKNKFLYSP-IANDVVKF-- 293  
 Db 243 IEKLNVN-PRHVGFKVLAFAFANRKFMLHDTVFTMDYDKFTTHPEIGDLRVFSV 301  
 QY 294 -WDYDLVNGGAEPQQLNGPLDKLASIINKEPV-LPIGGAGATEMEIARETNFDG 351  
 Db 302 TYENDTLHIEE-----HG-DLAELLAANGLKVELIRCQGDW--VAAGREQWNGSN 353  
 QY 352 YLAIKPGVIGYDRNEKTNAAKAGITVLPFHGNQLSLGNGNARCMSPILSKDV 407  
 Db 354 TLTAPGVVVYKNTITNAILESGKGLRLIKIGSELVGRGGRGPRCMSPFERDI 409

RESULT 15  
 ID\_ARCA\_BACLI STANDARD; PRT; 413 AA.  
 AC 086131, 2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD).  
 GN Name=arcA;  
 OS Bacillus licheniformis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1402;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 14580;  
 RC MEDLINE=99069319; PubMed=9851988;  
 RA Maghnoouj A., de Sousa Cabral T.F., Stalon V., Vander Wauven C.;  
 RT "The arcABDC gene cluster, encoding the arginine deiminase pathway of  
 RT Bacillus licheniformis, and its activation by the arginine repressor  
 RT argR.";  
 RL J. Bacteriol. 180:6468-6475(1998).  
 CC -!- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3).  
 CC -!- PATHWAY: Arginine degradation via arginine deiminase; first step.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -!- SIMILARITY: Belongs to the arginine deiminase family.  
 CC -----  
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 CC or send an email to license@sib-sib.ch).  
 CC -----

DR EMBL: Y17554; CAA76777.1; --  
 DR HAMAP: MF\_00242; -- 1.  
 DR InterPro: IPR003198; Amidino trans.  
 DR InterPro: IPR003876; Arg deiminase.  
 DR Pfam: PF02274; Amidinotransf. 1.  
 DR PRINTS: PR01466; ARGDEIMINASE.  
 DR TIGRFAMs: TIGR01078; arcA, 1.  
 DR Arginine metabolism; Hydrolase.  
 KW ACT\_SITE 402 402 Amidino-cysteine intermediate (By  
 FT similarity).  
 SQ SEQUENCE 413 AA; 47427 MW; 57BB97714CAA5480 CRC64;

Query Match 32.1%; Score 681.5; DB 1; Length 413;  
 Best Local Similarity 38.4%; Pred. No. 2.9e-38;  
 Matches 163; Conservative 66; Mismatches 152; Indels 43; Gaps 7;  
 QY 11 IHVYSEIGLETVLVEHGREIDYITPARLDELFSAILSHDARKEHQSFVKIMKDRGI 70  
 Db 7 IHVYSEIGPLKTVMLKRPGRLENLTPYELRLFFDDIPFLPAVQKEHQFAETLKQQA 66  
 QY 71 NVVELTDLVAETVDLASKAAKEEFTETLEETVPVLTANKKAVRAFLLSKPTHEMVFP 130  
 Db 67 EVLYLEKLAESALDDA--LVREQFIDELTESKADINGAYDR-LKEFLTLTFDADSNVEQV 123  
 QY 131 MSGITKYELGVSENEL-----IVDPNPNLYFTTRDPFASVGVNGVTIHFMRVIVR 180  
 Db 124 MSGIRKNELEKKEKSHLHLMEDHYPFLDPPNLYFTTRDPAAAGSGGUTINMKPEARR 183  
 QY 181 RETLFARFVRNHPKLIV--KTPWYDDPAMKPIEGDVFYINNETLVGVSVSRTDLDIT 238  
 Db 184 RESLFMRVIINHHPRFKGHEIPWLDLDRPKENIEGGDELVLNEETVAIGVSERTTAQAE 243  
 QY 239 LLAKNIKANKVEFKRIVAINVPKTNLMHLDITLMLDKNKFLYSPIANDVFKWDYDL 298  
 Db 244 RLVRNL-FORQSIIRRVLAVEIPKSRAPFMHLDITVFTMDRDQFTTHPAIQ----- 292  
 QY 299 VNGGAEPQQLNGPLDKLASIINKEPVLIP-----IGGAGATEMEIARE 344  
 Db 293 ---GPEGDMRIFFVLRGKTADSIHTTEHNLEVLKRTILGLSDVNLIFCGGDEIASARE 349  
 QY 345 TNFDGTNYLAIKPGLVIGYDRNEKTNAAKAGITVLPFHGNQLSLGNGNARCMSPILSR 404  
 Db 350 QWNDSNTLTAIPAGVVVTVYDRNYISNECLREQGKIVIEIPSGELSGRGGPRCMSPILYR 409  
 QY 405 KDVK 408  
 Db 410 EDVK 413

Search completed: November 23, 2004, 15:51:08  
 Job time : 195 secs